

(12) INTERNATIONAL APPLICATION PUBLISHED UNDER THE PATENT COOPERATION TREATY (PCT)

(19) World Intellectual Property
Organization
International Bureau



(43) International Publication Date
1 July 2004 (01.07.2004)

PCT

(10) International Publication Number
WO 2004/055181 A1

- (51) International Patent Classification⁷: C12N 15/00, C12Q 1/25, A01K 67/00
- (21) International Application Number: PCT/AU2003/001676
- (22) International Filing Date: 16 December 2003 (16.12.2003)
- (25) Filing Language: English
- (26) Publication Language: English
- (30) Priority Data:
2002953393 16 December 2002 (16.12.2002) AU
2003906285 14 November 2003 (14.11.2003) AU
- (71) Applicant (for all designated States except US): GARVAN INSTITUTE OF MEDICAL RESEARCH [AU/AU]; C/- St Vincent's Hospital, 384 Victoria Street, Darlinghurst, New South Wales 2010 (AU).
- (72) Inventors; and
- (75) Inventors/Applicants (for US only): MOLERO, Juan, Carlos [ES/AU]; 18/3 Bortfield Drive, Chiswick, New South Wales 2046 (AU). JAMES, David [AU/AU]; 25 Cutler Road, CLONTARF, New South Wales 2093 (AU).
- (81) Designated States (*national*): AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BW, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, EG, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NI, NO, NZ, OM, PG, PH, PL, PT, RO, RU, SC, SD, SE, SG, SK, SL, SY, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VC, VN, YU, ZA, ZM, ZW.
- (84) Designated States (*regional*): ARIPO patent (BW, GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW), Eurasian patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European patent (AT, BE, BG, CH, CY, CZ, DE, DK, EE, ES, FI, FR, GB, GR, HU, IE, IT, LU, MC, NL, PT, RO, SE, SI, SK, TR), OAPI patent (BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG).
- Published:
— with international search report
- For two-letter codes and other abbreviations, refer to the "Guidance Notes on Codes and Abbreviations" appearing at the beginning of each regular issue of the PCT Gazette.

(54) Title: METHODS OF TREATMENT OF FEEDING DISORDERS OR DISORDERS OF GLUCOSE UPTAKE AND FOR MODIFYING METABOLISM AND IDENTIFYING THERAPEUTIC REAGENTS THEREFOR

(57) Abstract: The present invention provides several assay formats for determining the effect of compounds on one or more metabolism-associated phenotypes in a cell, tissue or animal. The assay formats are based upon the finding that the proto-oncogene Cbl is involved in modulating basal glucose uptake, metabolic rate, adipogenesis, muscle thermogenesis, mitochondrial structure and function, the ratio of lean muscle mass to body fat and feeding behavior.

WO 2004/055181 A1

Methods of treatment of feeding disorders or disorders of glucose uptake and for
modifying metabolism and identifying therapeutic reagents therefor

Field of the invention

5 The present invention relates generally to the treatment of feeding disorders and disorders of glucose uptake or metabolism, such as, for example, diabetes, obesity, anorexia or bulimia, in humans and other animals. More particularly, this invention provides methods of modifying adipose tissue (e.g., in connection with
10 with treating overeating, bulimia or anorexia). The invention also relates to method for identifying modulators of glucose uptake or metabolism that are useful in the therapeutic methods described herein, e.g. using a non-human animal model.

Background to the invention

1. General

15 This specification contains nucleotide and amino acid sequence information prepared using PatentIn Version 3.1, presented herein after the claims. Each nucleotide sequence is identified in the sequence listing by the numeric indicator <210> followed by the sequence identifier (e.g. <210>1, <210>2, <213> etc). The length and type of sequence (DNA, protein (PRT), etc), and source organism for each
20 nucleotide sequence, are indicated by information provided in the numeric indicator fields <211>, <212> and <213>, respectively. Nucleotide sequences referred to in the specification are defined by the term "SEQ ID NO:", followed by the sequence identifier (eg. SEQ ID NO: 1 refers to the sequence in the sequence listing designated as <400>1).

25

The designation of nucleotide residues referred to herein are those recommended by the IUPAC-IUB Biochemical Nomenclature Commission, wherein A represents Adenine, C represents Cytosine, G represents Guanine, T represents thymine, Y represents a pyrimidine residue, R represents a purine residue, M
30 represents Adenine or Cytosine, K represents Guanine or Thymine, S represents Guanine or Cytosine, W represents Adenine or Thymine, H represents a nucleotide other than Guanine, B represents a nucleotide other than Adenine, V represents a

nucleotide other than Thymine, D represents a nucleotide other than Cytosine and N represents any nucleotide residue.

As used herein the term "derived from" shall be taken to indicate that a
5 specified integer may be obtained from a particular source albeit not necessarily directly from that source.

The embodiments of the invention described herein with respect to any single
embodiment shall be taken to apply *mutatis mutandis* to any other embodiment of the
10 invention described herein.

Throughout this specification, unless the context requires otherwise, the word
"comprise", or variations such as "comprises" or "comprising", will be understood to
imply the inclusion of a stated step or element or integer or group of steps or elements
15 or integers but not the exclusion of any other step or element or integer or group of
elements or integers.

Those skilled in the art will appreciate that the invention described herein is
susceptible to variations and modifications other than those specifically described. It is
20 to be understood that the invention includes all such variations and modifications. The
invention also includes all of the steps, features, compositions and compounds
referred to or indicated in this specification, individually or collectively, and any and all
combinations or any two or more of said steps or features.

25 The present invention is not to be limited in scope by the specific embodiments
described herein, which are intended for the purposes of exemplification only.
Functionally equivalent products, compositions and methods are clearly within the
scope of the invention, as described herein.

The present invention is performed without undue experimentation using,
30 unless otherwise indicated, conventional techniques of molecular biology,
microbiology, virology, recombinant DNA technology, peptide synthesis in solution,
solid phase peptide synthesis, and immunology. Such procedures are described, for
example, in the following texts that are incorporated by reference:

1. Sambrook, Fritsch & Maniatis, *Molecular Cloning: A Laboratory Manual*, Cold Spring Harbor Laboratories, New York, Second Edition (1989), whole of Vols I, II, and III;
2. DNA Cloning: A Practical Approach, Vols. I and II (D. N. Glover, ed., 1985), IRL Press, Oxford, whole of text;
3. Oligonucleotide Synthesis: A Practical Approach (M. J. Gait, ed., 1984) IRL Press, Oxford, whole of text, and particularly the papers therein by Gait, pp1-22; Atkinson *et al.*, pp35-81; Sproat *et al.*, pp 83-115; and Wu *et al.*, pp 135-151;
4. Nucleic Acid Hybridization: A Practical Approach (B. D. Hames & S. J. Higgins, eds., 1985) IRL Press, Oxford, whole of text;
5. Animal Cell Culture: Practical Approach, Third Edition (John R.W. Masters, ed., 2000), ISBN 0199637970, whole of text;
6. Immobilized Cells and Enzymes: A Practical Approach (1986) IRL Press, Oxford, whole of text;
7. Perbal, B., *A Practical Guide to Molecular Cloning* (1984);
8. *Methods In Enzymology* (S. Colowick and N. Kaplan, eds., Academic Press, Inc.), whole of series;
9. J.F. Ramalho Ortigão, "The Chemistry of Peptide Synthesis" *In: Knowledge database of Access to Virtual Laboratory website* (Interactiva, Germany);
10. Sakakibara, D., Teichman, J., Lien, E. and Fenichel, R.L. (1976). *Biochem. Biophys. Res. Commun.* **73** 336-342
11. Merrifield, R.B. (1963). *J. Am. Chem. Soc.* **85**, 2149-2154.
12. Barany, G. and Merrifield, R.B. (1979) in *The Peptides* (Gross, E. and Meienhofer, J. eds.), vol. 2, pp. 1-284, Academic Press, New York.
13. Wünsch, E., ed. (1974) *Synthese von Peptiden in Houben-Weyls Methoden der Organischen Chemie* (Müller, E., ed.), vol. 15, 4th edn., Parts 1 and 2, Thieme, Stuttgart.
14. Bodanszky, M. (1984) *Principles of Peptide Synthesis*, Springer-Verlag, Heidelberg.
15. Bodanszky, M. & Bodanszky, A. (1984) *The Practice of Peptide Synthesis*, Springer-Verlag, Heidelberg.
16. Bodanszky, M. (1985) *Int. J. Peptide Protein Res.* **25**, 449-474.

17. Handbook of Experimental Immunology, Vols. I-IV (D. M. Weir and C. C. Blackwell, eds., 1986, Blackwell Scientific Publications).

2. Description of the related art

5 The c-Cbl protein is a multi-adaptor protein that is involved in ligand-induced down regulation of receptor tyrosine kinases. The interaction between c-Cbl and its many binding partners involves particular c-Cbl protein domains. All Cbl proteins have a high degree of sequence homology between their tyrosine kinase-binding, linker and RING finger domains, and most have extensive proline-rich regions in their carboxy-
10 terminal halves. The tyrosine kinase-binding domain is composed of three interacting domains comprising a four-helix bundle, a Ca^{2+} -binding EF hand, and an atypical or variant Src homology region 2 (SH2) domain that is connected to the RING finger by a short linker domain. A ubiquitin-associated (UBA)/LZ domain at the carboxyl terminus of c-Cbl, Cbl-b and D-Cbl has homology to known ubiquitin-associated domains and
15 leucine zippers and is believed to be involved in Cbl-mediated ubiquitination of active receptors, which is essential for receptor degradation and turnover, thereby leading to cessation of downstream signalling from the receptor (Soubeyran *et al.*, *Nature* 416, 183-187, 2002).

20 Diabetes, and conditions related thereto such as obesity, are major health concerns throughout the world, and contribute to morbidity and mortality. Non-insulin dependent diabetes mellitus (NIDDM or type II diabetes), is the major form of diabetes in developed countries, however efficient means of therapeutic intervention are lacking. While a large number of environmental and genetic factors contribute to the
25 risk of NIDDM in the United States, prolonged obesity is by far the largest risk factor.

A variety of factors contribute to insulin resistance in laboratory animals, as well as in humans, including a sedentary lifestyle, a diet high in either fat or carbohydrate. A common feature of these risk factors is that the energy balance shifts
30 in favour of energy storage usually in the form of lipid. The intracellular accumulation of lipid is toxic to many cells such as pancreatic β -islet cells and this is considered to be an important factor in the progression of NIDDM.

To address these problems, the pharmaceutical industry has focused its efforts on identifying compounds that target a variety of metabolic endpoints, including insulin resistance, food intake and nutrient absorption. However, relatively few drugs have made it through clinical trials and most of these have unpleasant side effects. Insulin-sensitizing compounds that have been identified to target insulin resistance associated with both obesity and NIDDM often lead to increased body weight and so ultimately these may exacerbate some of the problems associated with these disorders. The insulin-sensitising compounds appear to increase adipocyte differentiation.

Before the development of diabetes, many obese patients develop a peripheral resistance to the actions of insulin. The molecular basis of insulin-resistance in obesity has been the subject of intensive study, but nonetheless remains elusive. Insights into components and mechanisms of the link between obesity and insulin resistance have been gained from mouse models of obesity which display obesity-induced insulin resistance. The molecular basis of the various mouse obesity models covers a range of mechanisms; nonetheless these all develop diabetes, either before or after the onset of obesity.

Obesity in humans and rodents is also commonly associated with insulin resistance in fat and muscle cells (LeRoith et al., *Diabetes Mellitus: a Fundamental and Clinical Text*, (Lippincott-Raven, Philadelphia, 1996); DeFronzo et al., *Diabetes Care* 15:318-68 (1992); Rifkin et al., *Diabetes Mellitus*, (Elsevier, N.Y., 1990)).

Much work has focussed on the insulin-sensitive glucose transporter GLUT4 (Watson and Pessin, *Exp. Cell Res.* 271: 75-83, 2001; Bogan et al. published U.S. Patent Application No. 20020052012). Insulin binds to the insulin receptor (IR) in the plasma membrane, where it activates tyrosine kinase in a cascade of events involving phosphatidylinositol 3-kinase (PI 3-K)-mediated recruitment of GLUT4 to the cell surface Min et al., *Mol. Cell.* 3: 751-760, 1999; Olson et al., *Mol. Cell. Biol.* 17: 2425-2435, 1997; Hausdorff et al., *J. Biol. Chem.* 270: 12965-12968, 1995; Elmendorf et al., *J. Biol. Chem.* 273: 13289-13296, 1998; Holman et al., *J. Biol. Chem.* 265: 18172-18179, 1990; Piper et al., *Am. J. Physiol.* 260: C570-C580). The activation of PI 3-K. However, PI-K3-mediated trafficking of GLUT4 is not sufficient to explain the extent of insulin resistance (Pessin et al., *J. Clin. invest.* 106: 165-169, 2000). For example,

other growth factors and adhesion molecules that can activate PI 3-K and its downstream kinases (ie. AKT, protein kinase C ζ / λ (PKC ζ / λ)) have no effect on glucose transport or GLUT4 translocation. Additionally, mutant mice lacking GLUT4 develop only mild hyperinsulinemia (Katz et al., Nature 377:151-155, 1995).

5

A second PI 3K-independent signalling cascade, initiated by recruitment of c-Cbl (Langdon et al., J. Virol. 63: 5420-5424, 1989; Langdon et al., Proc. Natl Acad. Sci. USA 86: 1168-1172, 1989) to the insulin receptor, has been postulated to be involved in insulin-stimulated glucose transport and uptake in fat and muscle cells. In this pathway, the c-Cbl protein is also recruited to the insulin receptor by interaction with the adaptor protein CAP, through one of three SH3 domains in the carboxyl-terminus of CAP. c-Cbl is then phosphorylated by the receptor, and the CAP-Cbl complex dissociates from the insulin receptor and moves to a caveolin-enriched triton insoluble membrane fraction. Based upon two-hybrid assay data measuring *in vitro* protein-protein associations Baumann et al., Nature 407: 202-207, 2000, showed that c-Cbl forms a ternary complex with two other proteins, CAP and flotillin. The interaction with flotillin directs the CAP-Cbl complex to the lipid raft sub-domain of the plasma membrane. Baumann et al. Nature 407: 202-207, 2000, also showed that both insulin-stimulated glucose transport and GLUT4 translocation to the cell surface are attenuated by about 50% in 3T3-L1 adipocytes by expression of a truncated CAP protein lacking SH3 domains (i.e. CAP Δ SH3). If this pathway were to operate in fat cells and/or muscle cells *in vivo*, it would be expected that insulin-induced glucose uptake and its subsequent incorporation into both glycogen and lipid would be impaired in situations which disrupt formation or activity of the c-Cbl-CAP-flotillin complex.

25

An interaction between c-Cbl and APS, an adaptor protein having a PH domain and SH2 domain (Ahmed et al., Biochem. J. 341, 665-668, 1999) is required for c-Cbl to bind to the insulin receptor in the caveolae-small invaginations in the plasma membrane that are a subset of the lipid raft domains. In this pathway, APS interacts with the phosphorylated insulin receptor via its SH2 domain, and subsequently undergoes tyrosine phosphorylation at a specific residue in the C-terminus of the protein. Upon phosphorylation, APS recruits c-Cbl to the receptor through an atypical SH2 domain of c-Cbl (Saltiel and Pessin, TRENDS Cell Biol. 12, 65-71, 2002).

30

Based upon co-localization studies, Chiang et al., Nature 410: 944-948, 2001 also showed that the time-course for the insulin-stimulated migration of c-Cbl parallels movement of the SH2-containing adaptor protein Crkl, and the guanyl nucleotide exchange factor C3G, into the caveolin-enriched triton insoluble membrane fraction. Chiang et al. also demonstrated that C3G exchanges GTP for GDP on TC10, a Rho-family GTP-binding protein that regulates GLUT4 transport. In this pathway, phosphorylated c-Cbl recruits Crkl to the lipid rafts, along with C3G to facilitate activation of TC10 by C3G (Chiang et al., Nature 410: 944-948, 2001).

10

No direct role for c-Cbl in modulating glucose uptake or GLUT4 translocation has been demonstrated in muscle and fat cells *in vivo*. This is because the binding studies by Baumann et al. and Chiang et al. *supra* were carried out in isolated 3T3L1 adipocytes and do not suggest that equivalent effects occur *in vivo*, let alone in both muscle and fat cells of animals. It is also unclear whether the effects reported by Baumann et al. for the over expression of CAP Δ SH3 protein in isolated adipocytes were a direct consequence of CAP failing to bind c-Cbl or to a secondary effect of expressing the mutant CAP Δ SH3 protein. For example, the expressed CAP Δ SH3 protein may have modified the ability of endogenous CAP to bind other proteins in the lipid rafts or elsewhere in the cell. Over expression of the CAP Δ SH3 protein also decreases insulin-stimulated recruitment of C3G into lipid rafts, and reduces the basal level of activated TC10 in 3T3-L1 adipocytes (Chiang et al., Nature 410: 944-948, 2001). Accordingly, no clear direct role has emerged for c-Cbl in modulating glucose uptake and incorporation into lipid in both fat cells and muscle cells of animals. Thus, it is not possible at present to conclude that impaired c-Cbl-CAP-flotillin complex formation and activity are sufficient to produce insulin resistance in humans and other animals.

A number of mouse models have been developed having genetic obesity-diabetes syndromes (Herberg, et al., Metabolism 26: 59-99, 1977). The mice typically have hyperglycemia, hyperinsulinemia, and obesity, albeit to different degrees, with different times of onset, and for different reasons. In the yellow obese mouse ($A^{y/a}$), a dominant mutation causes the ectopic, ubiquitous expression of the agouti protein, resulting in a condition similar to adult-onset obesity and non-insulin-dependent

diabetes mellitus (Michaud et al., Proc Natl Acad Sci USA 91: 2562-2566, 1994). Obese (ob/ob) (Zhang et al., Nature 372: 425-432, 1994); diabetes (db/db) (Tartaglia et al., Cell 83: 1263-1271, 1995), adipose (cpe/cpe) (Naggert et al., Nat. Genet. 10: 135-142, 1995) and tubby (tub/tub) (Kleyn et al., Cell 85: 281-290, 1996; Noben-
5 Trauth et al., Nature 380: 534-548, 1996) are mutations in the genes encoding leptin, the leptin receptor, carboxypeptidase E, and a member of a new family of genes encoding tubby-like proteins, respectively. Obese mice exhibit hyperglycemia, glucose intolerance, and elevated plasma insulin, which develops after the onset of obesity. In db/db mice, elevation of plasma insulin occurs at 2 weeks of age, preceding the onset
10 of obesity at 3-4 weeks and elevation of blood glucose levels at 4-8 weeks. Adipose mice have hyperinsulinemia throughout life in association with hypertrophy and hyperplasia of the islets of Langerhans, with transient hyperglycemia. Tubby mice have normal blood glucose, however plasma insulin is elevated prior to obvious signs of obesity, and the islets of Langerhans are enlarged.

15

Mouse models having impaired glucose uptake are highly desirable. By virtue of examining their phenotype, such models would have utility in determining appropriate targets for the therapy of a wide range of disorders associated with aberrant glucose metabolism, and for determining the efficacy or specificity of
20 therapeutics.

Summary of the invention

In work leading up to the present invention, the inventors studied the role of Cbl, particularly c-Cbl, in modulating one or more metabolism-associated phenotypes
25 in a cell, tissue or animal, e.g., in insulin resistance, obesity and diabetes *in vivo*. Surprisingly, the inventors found that a targeted disruption of a Cbl locus in mice sufficient to prevent functional Cbl protein from being expressed, does not disrupt, has little or no defect on basal or insulin-induced glucose uptake and incorporation of glucose into lipid in adipocytes. In muscle cells, Cbl-deficient mice were found to have
30 elevated basal glucose uptake, consistent with an enhanced metabolic rate. Cbl-deficient mice had significantly smaller adipocytes than wild-type counterparts of the same approximate weight. Consistent with this conclusion, the Cbl-deficient mice also had an elevated temperature relative to normal mice, suggesting that the enhanced ratio of lean muscle mass to body fat in Cbl-deficient mice is a consequence of

enhanced metabolic rate. It was also surprising that the feeding behavior of the animals was markedly modified, as Cbl-deficient mice exhibited a markedly enhanced appetite as determined by the amount of food consumed per day (dietary intake). These data also indicate that Cbl, such as, for example, c-Cbl, is directly involved in
5 modulating the feeding behavior of animals and in regulating fat deposition in adipocytes in mammals. The Cbl protein and Cbl-deficient mouse model are therefore useful for identifying compounds that specifically modulate a Cbl-mediated characteristic such as, for example, feeding behavior (e.g. in the treatment of anorexia or bulimia), fat deposition, metabolic rate, the ratio of lean muscle mass to body fat, or
10 glucose uptake (e.g. in the treatment of obesity or type II diabetes). These modulators are identified by screening animals for their effect on the phenotype of a suitable animal model, e.g., the Cbl^{-/-} mouse model or a derivative thereof expressing human c-Cbl protein, or alternatively, by directly screening the Cbl protein for altered function, including but not limited to any specific known functions of Cbl such as, for example,
15 binding activity, ubiquitin ligase activity, or by screening for the effect of the compound on the extent of tyrosine phosphorylation of Cbl.

Methods for determining the effect of a compound on a metabolism-associated phenotype of the mouse model will be apparent from the morphology and muscle
20 thermogenesis phenotypes described herein in Example 1-4. By "metabolism-associated phenotype" is meant a phenotype associated with Cbl activity and/or expression *per se* such as, for example, Cbl-mediated ubiquitination of the insulin receptor, tyrosine phosphorylation of Cbl, Cbl protein level, and/or Cbl-mediated fat and/or glucose metabolism, such as, for example, a phenotype selected from the
25 group consisting of fat mass, glucose transport, muscle thermogenesis, muscle temperature, mitochondrial structure, mitochondrial function, and mitochondrial respiration rate.

Accordingly, one aspect of the present invention provides a method of
30 identifying a compound that suppresses or reduces feeding behavior, such as, for example, in the treatment of obesity, said method comprising: (a) administering a compound to a genetically modified non-human animal comprising a genetic modification within an allele of its Cbl locus wherein said genetic modification reduces or prevents expression of a functional endogenous Cbl in said animal; and (b)

determining the feeding behavior of the animal, wherein reduced appetite or dietary intake of the animal compared to the appetite or dietary intake of a Cbl-deficient animal to which the compound has not been administered indicates that the compound suppresses or reduces feeding behavior.

5

In an alternative embodiment, the present invention provides a method for identifying a compound that suppresses or reduces feeding behavior, such as, for example, in the treatment of obesity, said method comprising determining the ubiquitin ligase activity of a Cbl protein in the presence and absence of the compound wherein
10 enhanced ubiquitin ligase activity of the Cbl protein in the presence of the compound indicates that the compound suppresses or reduces feeding behavior. In an alternative embodiment, the present invention provides a method for identifying a compound that suppresses or reduces feeding behavior comprising determining the level of tyrosine phosphorylation of a Cbl protein in the presence and absence of the compound
15 wherein enhanced phosphorylation of tyrosine residues in the Cbl protein in the presence of the compound indicates that the compound suppresses or reduces feeding behavior:

Another embodiment of the invention provides a method of identifying a
20 compound that enhances feeding behavior, such as, for example, in the treatment of anorexia or bulimia, said method comprising: (a) administering a compound that suppresses appetite or dietary intake to a genetically modified non-human animal comprising a genetic modification within an allele of its Cbl locus wherein said genetic modification reduces or prevents expression of a functional endogenous Cbl in said
25 animal and determining the feeding behavior of the animal; (b) administering a compound to the animal and determining the feeding behavior of the animal, wherein enhanced appetite or dietary intake at (b) compared to (a) indicates that the compound enhances feeding behavior.

30 In an alternative embodiment, the invention provides a method of identifying a compound that enhances feeding comprising determining the ubiquitin ligase activity of a Cbl protein in the presence and absence of the compound wherein reduced ubiquitin ligase activity of the Cbl protein in the presence of the compound indicates that the compound enhances feeding behavior.

In an alternative embodiment, the present invention provides a method for identifying a compound that enhances feeding behavior comprising determining the level of tyrosine phosphorylation of a Cbl protein in the presence and absence of the compound wherein reduced phosphorylation of tyrosine residues in the Cbl protein in the presence of the compound indicates that the compound enhances feeding behavior.

In an alternative embodiment, the invention provides a method of identifying a compound that modulates feeding behavior, such as, for example, in the treatment of anorexia or bulimia, said method comprising: (a) administering a compound to a non-human animal expressing a functional Cbl protein and determining the feeding behavior of the animal; (b) determining the feeding behavior of a genetically modified non-human animal comprising a genetic modification within an allele of its Cbl locus wherein said genetic modification reduces or prevents expression of a functional endogenous Cbl in said animal; and (c) comparing the feeding behavior of the animals at (a) and (b) wherein a comparable feeding behavior between (a) and (b) indicates that the compound modulates feeding behavior.

In the animal-based assays described herein, it is to be understood that the term "endogenous Cbl" refers to the Cbl encoded by the native genome of the animal, generally other than human Cbl.

In a particularly preferred embodiment of the present invention, an animal-based assay is employed utilizing a genetically modified animal that lacks expression of a functional endogenous Cbl and comprises a gene encoding human Cbl protein. Such animal models are particularly preferred for identifying a modulatory compound and/or for validating the efficacy of any compound or modulator identified using an animal-based assay (e.g., the Cbl^{-/-} mouse) or *in vitro* assay system. In particular, the use of an animal that ectopically expresses human Cbl protein or is capable of doing so permits the skilled artisan to determine that the compound or modulator targets the expression of the human Cbl gene or activity of the human Cbl protein, or is selective for human Cbl expression and/or activity.

In an alternative embodiment, the invention provides a method of identifying a compound that modulates feeding comprising determining the ubiquitin ligase activity of a Cbl protein in the presence and absence of the compound wherein modified ubiquitin ligase activity of the Cbl protein in the presence of the compound indicates
5 that the compound enhances feeding behavior.

In an alternative embodiment, the present invention provides a method for identifying a compound that modulates feeding behavior comprising determining the level of tyrosine phosphorylation of a Cbl protein in the presence and absence of the
10 compound wherein modified phosphorylation of tyrosine residues in the Cbl protein in the presence of the compound indicates that the compound modulates feeding behavior.

A further aspect of the present invention provides a method of identifying a
15 compound that enhances fat deposition or reduces lean muscle mass or enhances the ratio of body fat to muscle or reduces metabolic rate such as, for example, in the treatment of hypolipidemia (e.g. as observed in subjects suffering from abetalipoproteinemia, malnutrition or hematologic malignancies, such as acute myelocytic leukemia or chronic myelocytic leukemia), said method comprising: (a)
20 administering a compound to a genetically modified non-human animal comprising a genetic modification within an allele of its Cbl locus wherein said genetic modification reduces or prevents expression of a functional endogenous Cbl in said animal; and (b) determining the fat content of the animal, wherein enhanced fat content of the animal compared to the fat content of a Cbl-deficient animal to which the compound has not
25 been administered indicates that the compound enhances fat deposition or reduces lean muscle mass or enhances the ratio of body fat to muscle or reduces metabolic rate.

In an alternative embodiment, the present invention provides a method of
30 identifying a compound that enhances fat deposition or reduces lean muscle mass or enhances the ratio of body fat to muscle or reduces metabolic rate comprising determining the ubiquitin ligase activity of a Cbl protein in the presence and absence of the compound wherein enhanced ubiquitin ligase activity of the Cbl protein in the presence of the compound indicates that the compound enhances fat deposition or

reduces lean muscle mass or enhances the ratio of body fat to muscle or reduces metabolic rate.

In an alternative embodiment, the present invention provides a method for
5 identifying a compound that enhances fat deposition or reduces lean muscle mass or
enhances the ratio of body fat to muscle or reduces metabolic rate comprising
determining the level of tyrosine phosphorylation of a Cbl protein in the presence and
absence of the compound wherein enhanced phosphorylation of tyrosine residues in
the Cbl protein in the presence of the compound indicates that the compound
10 enhances fat deposition or reduces lean muscle mass or enhances the ratio of body
fat to muscle or reduces metabolic rate.

In an alternative embodiment, the invention provides a method of identifying a
compound that reduces fat deposition or enhances lean muscle mass or reduces the
15 ratio of body fat to muscle or enhances metabolic rate, such as, for example, in the
treatment of obesity or neurodegenerative disorders or for cosmetic purposes such as
bodybuilding or weight loss, said method comprising: (a) administering a compound
that enhances fat deposition or glucose uptake to a genetically modified non-human
animal comprising a genetic modification within an allele of its Cbl locus wherein said
20 genetic modification reduces or prevents expression of a functional endogenous Cbl in
said animal and determining the fat content of the animal; (b) administering a
compound to the animal and determining the fat content of the animal, wherein a
similar or reduced fat content at (b) compared to (a) indicates that the compound
reduces fat deposition or enhances lean muscle mass or reduces the ratio of body fat
25 to muscle or enhances metabolic rate.

In an alternative embodiment, the invention provides a method of identifying a
compound that reduces fat deposition or enhances lean muscle mass or reduces the
ratio of body fat to muscle or enhances metabolic rate comprising: (a) administering a
30 compound to a non-human animal expressing a functional Cbl protein and determining
the fat content of the animal; (b) determining the fat content of a genetically modified
non-human animal comprising a genetic modification within an allele of its Cbl locus
wherein said genetic modification reduces or prevents expression of a functional
endogenous Cbl in said animal; and (c) comparing the fat contents of the animals at

(a) and (b) wherein a comparable fat content between (a) and (b) indicates that the compound reduces fat deposition or enhances lean muscle mass or reduces the ratio of body fat to muscle or enhances metabolic rate.

5 In an alternative embodiment, the present invention provides a method of identifying a compound that reduces fat deposition or enhances lean muscle mass or reduces the ratio of body fat to muscle or enhances metabolic rate comprising determining the ubiquitin ligase activity of a Cbl protein in the presence and absence of the compound wherein reduced ubiquitin ligase activity of the Cbl protein in the
10 presence of the compound indicates that the compound reduces fat deposition or enhances lean muscle mass or reduces the ratio of body fat to muscle or enhances metabolic rate.

In an alternative embodiment, the present invention provides a method for
15 identifying a compound that reduces fat deposition or enhances lean muscle mass or reduces the ratio of body fat to muscle or enhances metabolic rate comprising determining the level of tyrosine phosphorylation of a Cbl protein in the presence and absence of the compound wherein reduced phosphorylation of tyrosine residues in the Cbl protein in the presence of the compound indicates that the compound reduces fat
20 deposition or enhances lean muscle mass or reduces the ratio of body fat to muscle or enhances metabolic rate.

A further aspect of the present invention provides a method of identifying a compound that enhances glucose uptake such as, for example, in the treatment of
25 hypolipidemia (e.g. as observed in subjects suffering from abetalipoproteinemia, malnutrition or hematologic malignancies, such as acute myelocytic leukemia or chronic myelocytic leukemia), said method comprising: (a) administering a compound to a genetically modified non-human animal comprising a genetic modification within an allele of its Cbl locus wherein said genetic modification reduces or prevents
30 expression of a functional endogenous Cbl in said animal; and (b) determining the glucose uptake into liver, fat or muscle cells of the animal, wherein enhanced uptake compared to the glucose uptake into liver, fat or muscle cells of a Cbl-deficient animal to which the compound has not been administered indicates that the compound enhances glucose uptake.

In an alternative embodiment, the present invention provides a method of identifying a compound that enhances glucose uptake comprising determining the ubiquitin ligase activity of a Cbl protein in the presence and absence of the compound
5 wherein reduced ubiquitin ligase activity of the Cbl protein in the presence of the compound indicates that the compound reduces fat deposition or enhances glucose uptake.

In an alternative embodiment, the present invention provides a method for
10 identifying a compound that enhances glucose uptake comprising determining the level of tyrosine phosphorylation of a Cbl protein in the presence and absence of the compound wherein reduced phosphorylation of tyrosine residues in the Cbl protein in the presence of the compound indicates that the compound enhances glucose uptake.

15 In an alternative embodiment, the invention provides a method of identifying a compound that reduces glucose uptake into liver, fat or muscle cells such as, for example, in the treatment of obesity; said method comprising: (a) administering a compound that enhances glucose uptake to a genetically modified non-human animal comprising a genetic modification within an allele of its Cbl locus wherein said genetic
20 modification reduces or prevents expression of a functional endogenous Cbl in said animal and determining the glucose uptake into liver, fat or muscle cells; (b) administering a compound to the animal and determining the glucose uptake into liver, fat or muscle cells of the animal, wherein a similar or reduced uptake at (b) compared to (a) indicates that the compound reduces glucose uptake into liver, fat or muscle
25 cells.

In an alternative embodiment, the invention provides a method of identifying a compound that reduces glucose uptake into liver, fat or muscle cells comprising: (a) administering a compound to a non-human animal expressing a functional Cbl protein
30 and determining the glucose uptake into liver, fat or muscle cells of the animal; (b) determining the glucose uptake into liver, fat or muscle cells of a genetically modified non-human animal comprising a genetic modification within an allele of its Cbl locus wherein said genetic modification reduces or prevents expression of a functional endogenous Cbl in said animal; and (c) comparing the glucose uptake into liver, fat or

muscle cells of the animals at (a) and (b) wherein a comparable uptake between (a) and (b) indicates that the compound reduces glucose uptake into liver, fat or muscle cells.

5 In an alternative embodiment, the present invention provides a method of identifying a compound that reduces glucose uptake comprising determining the ubiquitin ligase activity of a Cbl protein in the presence and absence of the compound wherein enhanced ubiquitin ligase activity of the Cbl protein in the presence of the compound indicates that the compound reduces glucose uptake.

10

In an alternative embodiment, the present invention provides a method for identifying a compound that reduces glucose uptake comprising determining the level of tyrosine phosphorylation of a Cbl protein in the presence and absence of the compound wherein enhanced phosphorylation of tyrosine residues in the Cbl protein in
15 the presence of the compound indicates that the compound reduces glucose uptake.

In a particularly preferred embodiment of the screening assay, the present invention provides a method of identifying a compound that is capable of modulating feeding behavior, fat deposition, metabolic rate, or the ratio of lean muscle mass to
20 body fat in a subject, said method comprising performing an assay to measure a metabolism-associated phenotype that has been determined for a genetically modified non-human animal that comprises a genetic modification within an allele of its Cbl locus wherein said genetic modification reduces or prevents expression of a functional endogenous Cbl in said animal, and wherein said assay is conducted in the presence
25 and absence of a compound to be tested, and determining the effect of the compound on the phenotype wherein a modified phenotype indicates that the compound is capable of modulating feeding behavior, fat deposition, metabolic rate, or the ratio of lean muscle mass to body fat in a subject.

30 In one embodiment, the assay to determine a metabolism-associated phenotype measures Cbl-mediated ubiquitination of the insulin receptor in the presence and absence of the compound. Preferably, the assay comprises:

- (a) providing a cell that is capable of effecting the c-Cbl-mediated ubiquitination of the insulin receptor;

- (b) incubating the cell in the presence and absence of a compound to be tested; and
- (c) determining c-Cbl-mediated ubiquitination of the insulin receptor in the presence and absence of the compound wherein a modified level of c-Cbl-mediated ubiquitination of the insulin receptor indicates that the compound is capable of modulating feeding behavior, fat deposition, metabolic rate, or the ratio of lean muscle mass to body fat in a subject.

Preferably, the compound reduces or inhibits Cbl-mediated ubiquitination of the insulin receptor thereby indicating that said compound is capable of enhancing feeding behavior in a subject, reducing fat deposition in a subject, enhancing metabolic rate in a subject, or enhancing the ratio of lean muscle mass to body fat in a subject.

Alternatively, the compound enhances or agonizes Cbl-mediated ubiquitination of the insulin receptor thereby indicating that said compound is capable of reducing feeding behavior and/or enhancing fat deposition in a subject and/or reducing metabolic rate in a subject and/or reducing the ratio of lean muscle mass to body fat in a subject.

In a particularly preferred embodiment, the assay comprises an immunoassay wherein the level of c-Cbl-mediated ubiquitination of the insulin receptor is determined by contacting the insulin receptor with an antibody that binds to ubiquitin under conditions sufficient for an antigen-antibody complex to form and detecting the antibody bound to the receptor. Preferably, the assay further comprises contacting the insulin receptor with an antibody that binds to the insulin receptor under conditions sufficient for an antigen-antibody complex to form.

In an alternative embodiment, the method comprises performing an immunoassay by a process comprising:

- (a) providing a cell that is capable of effecting the c-Cbl-mediated ubiquitination of the insulin receptor;
- (b) incubating the cell in the presence and absence of a compound to be tested;

- (c) contacting an extract of the cell comprising the insulin receptor with an antibody that binds to the insulin receptor under conditions sufficient for an antigen-antibody complex to form thereby capturing the insulin receptor;
- (d) contacting the captured insulin receptor with an antibody that binds to ubiquitin under conditions sufficient for an antigen-antibody complex to form; and
- (e) detecting the antibody bound at (d).

In accordance with this embodiment, the antibody bound at (d) is generally detected by contacting the antibody with a tertiary antibody that is capable of producing a detectable signal.

10

In a further embodiment of the present invention, the assay to determine a metabolism-associated phenotype measures phosphorylation of a tyrosine residue on Cbl protein in the presence and absence of the compound.

15 In a further embodiment of the present invention, the assay to determine a metabolism-associated phenotype measures the amount of Cbl protein in the cell in the presence and absence of the compound. Preferred assay formats in accordance with this embodiment comprise:

- (a) providing a cell that is capable of expressing c-Cbl protein;
- 20 (b) incubating the cell in the presence and absence of a compound to be tested; and
- (c) determining amount of c-Cbl protein in the cell in the presence and absence of the compound wherein a modified level of c-Cbl protein indicates that the compound is capable of modulating feeding behavior, fat deposition, metabolic rate, or the ratio of lean muscle mass to body fat in a subject.

25

Preferably, a compound that reduces or inhibits Cbl expression as determined by a reduced amount of Cbl protein in the cell is capable of enhancing feeding behavior, reducing fat deposition, enhancing metabolic rate, or enhancing the ratio of lean muscle mass to body fat in a subject.

30

Alternatively, a compound that enhances or agonizes Cbl expression as determined by an increased amount of Cbl protein in the cell is capable of reducing feeding behavior and/or enhancing fat deposition in a subject and/or reducing

metabolic rate in a subject and/or reducing the ratio of lean muscle mass to body fat in a subject.

In a particularly preferred embodiment, the amount of Cbl protein in a cell is
5 determined by performing an immunoassay wherein the amount of c-Cbl is determined
by contacting the Cbl protein with an antibody that binds to Cbl under conditions
sufficient for an antigen-antibody complex to form and detecting the antibody bound to
the Cbl protein. Preferably, the antibody bound to the Cbl protein is detected by
contacting the antibody with a secondary antibody that is capable of producing a
10 detectable signal.

In an alternative embodiment, an immunoassay is performed wherein the
amount of c-Cbl is determined by contacting the Cbl protein with a primary and
secondary antibody that each bind to Cbl under conditions sufficient for antigen-
15 antibody complexes to form and detecting an antibody bound to the Cbl protein. The
antibody bound to the Cbl protein is generally detected by contacting the antibody with
a secondary antibody that is capable of producing a detectable signal. The primary
and secondary antibody will generally bind to different epitopes on the Cbl protein.

20 In a further embodiment, the amount of Cbl protein in a cell is detected by an
immunoassay comprising:

- (a) providing a cell that is capable of expressing c-Cbl protein;
- (b) incubating the cell in the presence and absence of a compound to be tested;
- (c) contacting an extract of the cell comprising the Cbl protein with an antibody
25 that binds to Cbl protein under conditions sufficient for an antigen-antibody
complex to form thereby capturing the Cbl protein; and
- (d) detecting the antibody bound at (e).

In a further embodiment, the amount of Cbl protein in a cell is detected by an
30 immunoassay comprising:

- (a) providing a cell that is capable of expressing c-Cbl protein;
- (b) incubating the cell in the presence and absence of a compound to be tested;

- (c) contacting an extract of the cell comprising the Cbl protein with an antibody that binds to Cbl protein under conditions sufficient for an antigen-antibody complex to form thereby capturing the Cbl protein;
- (d) contacting the captured Cbl protein with an antibody that binds to Cbl protein under conditions sufficient for an antigen-antibody complex to form, wherein said antibody binds to a different epitope on Cbl to the antibody at (c); and
- (e) detecting the antibody bound at (d).

As with these and other preferred immunoassays, the antibody is generally detected by contacting the antibody with an antibody that is capable of producing a detectable signal.

In a further embodiment of the present invention, the assay to determine a metabolism-associated phenotype measures Cbl-mediated fat and/or glucose metabolism in the cell in the presence and absence of the compound. Preferably, the assay to determine a metabolism-associated phenotype measures a phenotype in the presence and absence of the compound selected from the group consisting of fat mass, glucose transport, muscle thermogenesis, mitochondrial structure, mitochondrial function, and mitochondrial respiration rate. Preferably, these parameters are measured in a cell, tissue or animal in the presence and absence of the compound.

As exemplified herein, muscle thermogenesis e.g., in the presence and absence of a test compound, is determined by a process comprising determining the proton leak kinetics of a cell. Accordingly, one particularly preferred embodiment of the measurement of muscle thermogenesis in a cell comprises:

- (a) providing a cell of myoblast lineage capable of expressing c-Cbl protein;
- (b) incubating the cell in the presence and absence of a compound to be tested; and
- (c) determining the respiration rate and/or membrane potential of the cell in the presence and absence of the compound wherein a modified respiration rate and/or membrane potential indicates that the compound is capable of modulating feeding behavior, fat deposition, metabolic rate, or the ratio of lean muscle mass to body fat in a subject.

In accordance with this embodiment, those compounds that enhance respiration rate and/or membrane potential of a cell are capable of enhancing feeding behavior, reducing fat deposition, enhancing metabolic rate, or enhancing the ratio of lean muscle mass to body fat in a subject.

5

In contrast, compounds that reduce or inhibit respiration rate and/or membrane potential of the cell are capable of reducing feeding behavior and/or enhancing fat deposition in a subject and/or reducing metabolic rate in a subject and/or reducing the ratio of lean muscle mass to body fat in a subject.

10

In a particularly preferred embodiment, animal models are used to test or validate a putative modulatory compound. In one embodiment, an assay that determines the effect of a compound on a metabolism-associated phenotype comprises:

- 15 (a) providing a compound to be tested to an animal subject that expresses a functional Cbl protein; and
- (b) determining a metabolism-associated phenotype in a cell or tissue of the animal wherein a modified phenotype in the presence of the compound indicates that the compound is capable of modulating feeding behavior, fat
20 deposition, metabolic rate, or the ratio of lean muscle mass to body fat in a subject.

20

Preferably, the metabolism-associated phenotype measured as the assay read-out is selected from the group consisting of fat mass, glucose transport, muscle
25 thermogenesis, mitochondrial structure, mitochondrial function, and mitochondrial respiration rate. As with other embodiments described herein, muscle thermogenesis in the presence of the compound is preferably determined by a process comprising determining the proton leak kinetics of a cell or tissue of the animal. More preferably, muscle thermogenesis is determined by measuring the respiration rate and/or
30 membrane potential of a cell from the animal wherein a modified respiration rate and/or membrane potential indicates that the compound is capable of modulating feeding behavior, fat deposition, metabolic rate, or the ratio of lean muscle mass to body fat in a subject.

In accordance with this embodiment, a compound that enhances respiration rate and/or membrane potential of the cell is capable of enhancing feeding behavior, reducing fat deposition, enhancing metabolic rate, or enhancing the ratio of lean muscle mass to body fat in a subject.

5

In contrast, a compound that reduces or inhibits respiration rate and/or membrane potential of the cell thereby indicating that said compound is capable of reducing feeding behavior and/or enhancing fat deposition in a subject and/or reducing metabolic rate in a subject and/or reducing the ratio of lean muscle mass to body fat in
10 a subject.

It is particularly preferred that the animal subject used in the screens provided by the present invention is a non-human animal subject, preferably a mammal, such as; for example, a rodent (e.g., a rabbit, rat, guinea pig or mouse), dog, pig, bovine,
15 sheep, horse and goat etc., and more preferably a rabbit, rat or mouse.

In one embodiment, the non-human animal subject expresses an endogenous native Cbl protein (i.e. it is a wild-type animal with respect to Cbl expression). The present invention clearly provides for the use of a Cbl-knock-in animal that expresses
20 an introduced human Cbl protein.

Preferably, a test compound is administered to muscle tissue of the animal subject. In the case of nucleic acids, it is particularly preferred that these are provided by injection. Preferably, the nucleic acids are contained within a virus vector, in
25 particular an adenovirus. As will be known to those skilled in the art, such adenoviruses tend to remain localized to the injection site. Accordingly, the metabolism-associated phenotype will generally be determined in muscle tissue of the animal subject to which the virus vector is administered.

30 A further aspect of the present invention provides methods for determining a modulator of the activity, formation or stability of a protein complex selected from the group consisting of: (i) a Cbl-APS complex; (ii) a Cbl-CAP complex; (iii) a Cbl-CAP-flotillin complex; (iv) a Cbl- C3G complex; (v) a Cbl-CrkII complex; and (vi) a Cbl-C3G-CrkII complex.

The present invention clearly encompasses the use of any *in silico* analytical method and/or industrial process for carrying the screening methods described herein into a pilot scale production or industrial scale production of an inhibitory compound identified in such screens. This invention also provides for the provision of information for any such production. Accordingly, a further aspect of the present invention provides a process for identifying or determining a compound or modulator *supra*, said method comprising:

- (i) performing a method as described herein to thereby identify or determine a compound or modulator;
- (ii) optionally, determining the structure of the compound or modulator; and
- (iii) providing the compound or modulator or the name or structure of the compound or modulator such as, for example, in a paper form, machine-readable form, or computer-readable form.

Naturally, for compounds that are known albeit not previously tested for their function using a screen provided by the present invention, determination of the structure of the compound is implicit in step (i) *supra*. This is because the skilled artisan will be aware of the name and/or structure of the compound at the time of performing the screen.

As used herein, the term "providing the compound or modulator" shall be taken to include any chemical or recombinant synthetic means for producing said compound or modulator or alternatively, the provision of a compound or modulator that has been previously synthesized by any person or means.

In a preferred embodiment, the compound or modulator or the name or structure of the compound or modulator is provided with an indication as to its use e.g., as determined by a screen described herein.

A further aspect of the present invention provides a process for producing a compound or modulator *supra*, said method comprising:
a process for identifying or determining a compound or modulator *supra*, said method comprising:

- (i) performing a method as described herein to thereby identify or determine a compound or modulator;

- (ii) optionally, determining the structure of the compound or modulator;
- (iii) optionally, providing the name or structure of the compound or modulator such as, for example, in a paper form, machine-readable form, or computer-readable form; and
- 5 (iv) producing or synthesizing the compound or modulator.

In a preferred embodiment, the synthesized compound or modulator or the name or structure of the compound or modulator is provided with an indication as to its use e.g., as determined by a screen described herein.

10

In a further aspect, the invention provides methods relating to the treatment of animal or human subjects wherein a compound that modulates (i.e. enhances or reduces or prevents) Cbl expression or activity is administered to the animal. Such methods apply *mutatis mutandis* to the treatment of a wide range of conditions
15 associated with Cbl function, such as, for example, hyperglycemia, hyperinsulinemia, obesity, adult-onset obesity, non-insulin-dependent diabetes mellitus, type II diabetes, glucose intolerance, hypertrophy or hyperplasia of the islets of Langerhans, or for cosmetic purposes, such as, for example, bodybuilding or weight management (i.e. weight loss or weight gain). It is to be understood that such applications of the
20 invention also relate to the productivity of stock and farm animals (e.g. dairy and beef cattle, pigs, horses, sheep, etc) such as, for example, for modulating the amount of fat they deposit or their ratio of fat to muscle mass. In accordance with this aspect of the invention, an amount of a Cbl agonist or antagonist is administered to the animal or human subject effective to modulate the expression or activity of Cbl in the subject.

25

In another embodiment, the invention also provides a method of treating a feeding disorder characterized by reduced dietary intake or suppressed appetite in a subject said method comprising administering to the subject an amount of a Cbl antagonist effective to enhance the appetite or dietary intake of the subject. The
30 method of the invention is particularly suited to the treatment of anorexia or bulimia.

In a related embodiment, the invention also provides a method of treating a feeding disorder characterized by reduced dietary intake or suppressed appetite in a subject said method comprising administering to the subject an amount of a compound

that reduces expression of functional Cbl effective to enhance the appetite or dietary intake of the subject.

Brief description of the drawings

5 Figure 1 is a graphical representation showing the body weight in grams (ordinate) of male (circles) and female (triangles) wild type mice (open symbols), and Cbl-deficient male (circles) and female (triangles) mice that are homozygous for a mutation in both alleles of the Cbl locus (filled symbols). Body weights of mice were determined every week from weaning to 16 weeks of age (x-axis). Data indicate that
10 Cbl-deficient male mice have significantly higher body weight than their wild-type counterparts, throughout the time period tested. The weights of Cbl-deficient female mice are comparable to the weights of wild-type females.

Figure 2 is a graphical representation showing the dietary food intake in grams
15 per day (ordinate) of male (circles) and female (triangles) wild type mice (open symbols), and Cbl-deficient male (circles) and female (triangles) mice that are homozygous for a mutation in both alleles of the Cbl locus (filled symbols). Food intake was determined every week from 5 weeks of age until 16 weeks of age (x-axis). Data indicate that Cbl-deficient male and female mice have significantly enhanced
20 dietary intake (i.e. enhanced appetite) than their wild-type counterparts, throughout the time period tested. The dietary intake of Cbl-deficient female mice is also significantly higher than the dietary intake of wild-type males.

Figure 3 is a graphical representation showing the dietary food intake relative
25 to body weight (ordinate) of male (circles) and female (triangles) wild type mice (open symbols), and Cbl-deficient male (circles) and female (triangles) mice that are homozygous for a mutation in both alleles of the Cbl locus (filled symbols). Food intake relative to body weight was determined every week from 5 weeks of age until 16 weeks of age (x-axis). Data indicate that Cbl-deficient male and female mice have
30 significantly enhanced specific dietary intake (i.e. enhanced appetite as determined by food intake relative to body weight) than their wild-type counterparts, throughout the time period tested.

Figure 4 is a tabular representation showing the tissue weights (average \pm SEM) of wild type mice and Cbl-deficient mice that are homozygous for a mutation in both alleles of the Cbl locus (filled symbols). WAT, white adipose tissue; BAT, brown adipose tissue; QUAD, quadriceps muscle. Data indicate reduced adipose tissue weight for Cbl-deficient animals relative to wild type animals.

Figure 5 is a photographic representation showing adipocyte size in wild type mice (left) and Cbl-deficient mice that are homozygous for a mutation in both alleles of the Cbl locus (right).

Figure 6 is a tabular representation showing adipocyte diameter (μm) adipocyte volume (pl/cell) and lipid content (ng/cell) of male (Top panel) and female (Lower panel) wild type mice (WT), compared to male (Top panel) and female (Lower panel) Cbl-deficient mice that are homozygous for a mutation in both alleles of the Cbl locus (KO). Data indicate the mean values \pm SEM. Data indicate that for both males and females, there is a significant reduction in adipocyte size and volume, and reduced lipid content of adipocytes in Cbl-deficient mice relative to wild-type mice.

Figure 7A is a graphical representation showing glucose transport in soleus muscles of c-CBL⁺ mice. Soleus muscles were removed from c-CBL^{-/-} mice and wild-type c-CBL^{+/+} mice and incubated in the presence of labeled 2-deoxyglucose and no insulin (basal), 300 $\mu\text{U}/\text{ml}$ insulin (submax) and 1000 $\mu\text{U}/\text{ml}$ insulin (supramax). The muscle was then liquefied and the amount of labeled 2-deoxyglucose taken up by the muscle determined using a liquid scintillation counter. This amount \pm SEM was then graphically represented. *, $p < 0.05$; *, $p < 0.01$.

Figure 7B is a graphical representation showing glucose transport in extensor digitorum longus muscles of c-CBL⁺ mice. Extensor digitorum longus muscles were removed from c-CBL^{-/-} mice and wild-type c-CBL^{+/+} mice and incubated in the presence of labeled 2-deoxyglucose and no insulin (basal), 300 $\mu\text{U}/\text{ml}$ insulin (submax) and 1000 $\mu\text{U}/\text{ml}$ insulin (supramax). The muscle was then liquefied and the amount of labeled 2-deoxyglucose taken up by the muscle determined using a liquid scintillation counter. This amount \pm SEM was then graphically represented. *, $p < 0.05$.

Figure 8 is a graphical representation showing glucose transport in fat explants taken from c-CBL^{-/-} mice. Epididymal fat pads removed from c-CBL^{-/-} mice and wild-type c-CBL^{+/+} mice and minced. Samples were then incubated in the presence of labeled 2-deoxyglucose and no insulin (0), 0.05nM insulin (0.05) and 1nM insulin (1).

5 The amount of labeled 2-deoxyglucose taken up by the fat explant was determined using a liquid scintillation counter. This amount +/- SEM was then graphically represented.

10 Detailed description of the Preferred embodiments

One aspect of the present invention provides a method of identifying a compound that suppresses or reduces feeding behavior, such as, for example, in the treatment of obesity, said method comprising: (a) administering a compound to a genetically modified non-human animal comprising a genetic modification within an
15 allele of its Cbl locus wherein said genetic modification reduces or prevents expression of a functional endogenous Cbl in said animal; and (b) determining the feeding behavior of the animal, wherein reduced appetite or dietary intake of the animal compared to the appetite or dietary intake of a Cbl-deficient animal to which the compound has not been administered indicates that the compound suppresses or
20 reduces feeding behavior.

As used herein, the term "Cbl" shall be taken to mean any peptide, polypeptide, or protein having at least about 80% amino acid sequence identity to the amino acid sequence of a human or mouse c-Cbl polypeptide set forth in SEQ ID NO: 2 or 3. The
25 term "Cbl" shall also be taken to include a peptide, polypeptide or protein having the known biological activity of Cbl, or the known binding specificity of Cbl including c-Cbl. For the purposes of nomenclature, the amino acid sequences of the murine and human Cbl polypeptides are exemplified herein, as SEQ ID Nos: 2 and 3, respectively. Preferably, the percentage identity to SEQ ID NO: 2 or 3 is at least about 85%, more
30 preferably at least about 90%, even more preferably at least about 95% and still more preferably at least about 99%.

A "Cbl" protein generally comprises about 906 amino acid residues in length. The full-length protein generally comprises a tyrosine kinase binding domain that binds

the protein to phosphotyrosine residues, thereby coupling Cbl to growth factor receptor signalling. For example, the c-Cbl is phosphorylated on 3-4 tyrosine residues in response to growth factors, the phosphorylated residues representing binding domains for SH2 domain containing proteins such as PI 3' kinase and Crk II. The tyrosine
5 kinase binding domain generally will comprise a four helix bundle, an EF hand domain and an SH2 domain. Downstream of the tyrosine kinase binding domain is generally a C3HC4 RING finger domain having high sequence similarity to that found in ubiquitin ligase proteins. At the C terminal portion of the protein there is generally a proline rich region (PRR) which can bind SH3 domain-containing proteins (e.g. CAP). At the
10 extreme C terminus of Cbl there is generally located a leucine zipper domain (b-Zip) and a ubiquitin association domain that regulates homodimerization of Cbl.

The various embodiments of the present invention directed to the identification of compounds that modulate feeding behavior (e.g. in the treatment of obesity,
15 anorexia or bulimia), fat deposition, metabolic rate, the ratio of lean muscle mass to body fat, or glucose uptake (e.g. in the treatment of obesity or type II diabetes), can also be carried out by determining a physical property of the Cbl protein, or alternatively, a catalytic activity of the Cbl protein, that is modified during glucose uptake into fat cells or muscle cells.

20

The ability of a compound to enhance feeding behavior, reduce fat deposition, enhance metabolic rate, or enhance the ratio of lean muscle mass to body fat can thus be readily assayed by determining whether or not the compound reduces a Cbl activity that is disrupted in the Cbl-deficient mouse model. For example, reduced ubiquitin
25 ligase activity of Cbl protein, or reduced phosphorylation of tyrosine residues in the Cbl protein (e.g. linked to growth receptor-mediated signalling events such as by measuring cAMP-mediated phosphorylation), or reduced binding of Cbl to an SH3-containing protein, would indicate the ability of a compound to produce these effects. Standard assays for determining tyrosine phosphorylation of Cbl, receptor-mediated
30 signalling of tyrosine phosphorylation in Cbl protein, ubiquitin ligase activity of Cbl or binding of Cbl to SH3 domains, are known to the skilled artisan.

Similarly, the ability of a compound to reduce feeding behavior, enhance fat deposition, reduce metabolic rate, or enhance the ratio of body fat to lean muscle

mass can be assayed by determining whether or not the compound enhances ubiquitin ligase activity of Cbl protein, or enhances phosphorylation of tyrosine residues in the Cbl protein (e.g. linked to growth receptor-mediated signaling events such as by measuring cAMP-mediated phosphorylation), or enhances binding of Cbl to
5 an SH3-containing protein.

By "Cbl-deficient" is meant that insufficient functional Cbl protein is produced to facilitate the level of glucose uptake or glycogen synthesis or lipogenesis detected in a wild type animal that does not suffer from a disorder of glucose metabolism. Glucose
10 uptake, glycogen synthesis, or lipogenesis can readily be determined using known methods, such as, for example, by determining 2-deoxyglucose uptake into isolated liver, fat or muscle cells and/or glycogen synthesis and/or lipogenesis in the presence and absence of insulin as described by Lazar et al., J. Biol. Chem. 270: 20801-20807, 1995.

15 Preferably, the Cbl deficiency causes reduced Cbl expression at least in liver, fat or muscle cells of the genetically modified animal, more preferably in a tissue selected from the group consisting of adipose, skeletal muscle and cardiac muscle. Effects on Cbl expression in other cells or tissues, such as, for example, immune cells
20 or brain, are not to be excluded from the scope of the present invention.

In one embodiment, the genetic modification capable of producing the Cbl deficient phenotype is selected from the group consisting of a deletion, an insertion, a substitution and an inversion of nucleotides in an allele of the Cbl locus. In another
25 embodiment, the genetic modification is a deletion of a nucleotide sequence within two alleles of the Cbl locus, wherein the deletion results in an absence of expression of a functional or full-length Cbl protein by the animal. In a particularly preferred embodiment, the genetic modification comprises the deletion of a nucleotide sequence encoding a protein-encoding portion of the Cbl gene sufficient to prevent Cbl function,
30 or alternatively, the introduction of an in-frame stop codon at a location in the protein-encoding portion of the Cbl gene sufficient to prevent expression of functional Cbl by one or both Cbl-encoding alleles. Even more preferably, the genetic modification comprises the targeted disruption of one or two alleles at the Cbl locus produces a truncated Cbl protein comprising the amino acid sequence set forth in SEQ ID NO: 1.

Preferably, the genetic modification is in both alleles of the Cbl locus (i.e. the animal is homozygous for the genetic modification).

- 5 The non-human animal is any mammal, such as, for example, a rodent, dog, pig, bovine, sheep, horse or goat. In one embodiment, the animal is a rodent selected from the group consisting of rabbit, rat, guinea pig and mouse. Conveniently, the animal is a mouse.
- 10 The Cbl-deficient "control" animal employed in this context can be any other animal that has reduced expression of Cbl expression and need not be isogenic to the animal on which the compound was tested (i.e. the "test" animal). Preferably, the control and test animals express similar levels of functional Cbl. More preferably, the control and test animals are isogenic. Preferably, the appetite or dietary intake of the
- 15 animal is modified to a level that is comparable to the appetite or dietary intake of a wild-type animal and does not completely suppress appetite or dietary intake if the animal.

By "feeding behavior" is meant appetite or the amount of food consumption of the animal in a particular time interval, or its dietary intake expressed in absolute terms or alternatively, as a proportion of total body mass. Dietary intake will also be generally determined relative to a particular time interval (e.g. per hour, per day, etc). In most non-human animals, dietary intake is the preferred measure.

- 25 The range of compounds contemplated herein for modulating feeding behavior include peptides, including peptides derived from Cbl and capable of complementing the Cbl-deficiency; non-Cbl peptides, such as, for example Cbl peptidomimetics; small organic molecules, such as, for example derived from publicly available combinatorial libraries; and nucleic acids, including nucleic acid encoding said peptide derived from
- 30 Cbl or said non-Cbl peptide.

In one embodiment, the subject method further comprises formulating the identified compound for administration to a non-human animal or a human. The formulations can be suitable for administration by injection by a subcutaneous,

intravenous, intranasal, or intraperitoneal route. Alternatively, they can be suitable for oral administration in the form of feed additives, tablets, troches, etc.

The compounds are conveniently formulated in a suitable excipient or diluent, such as, for example, an aqueous solvent, non-aqueous solvent, non-toxic excipient, such as a salt, preservative, buffer and the like. Examples of non-aqueous solvents are propylene glycol, polyethylene glycol, vegetable oil and injectable organic esters such as ethyloleate. Aqueous solvents include water, alcoholic/aqueous solutions, saline solutions, parenteral vehicles such as sodium chloride, Ringer's dextrose, etc.

Preservatives include antimicrobial, anti-oxidants, chelating agents and inert gases. The pH and exact concentration of the various components the formulation suitable for administration to the animal are adjusted according to routine skills in the art. Solutions or suspensions used for parenteral, intradermal, or subcutaneous application can include the following components: a sterile diluent such as water for injection, saline solution, fixed oils, polyethylene glycols, glycerine, propylene glycol or other synthetic solvents; antibacterial agents such as benzyl alcohol or methyl parabens; antioxidants such as ascorbic acid or sodium bisulfite; chelating agents such as ethylenediaminetetraacetic acid; buffers such as acetates, citrates or phosphates and agents for the adjustment of tonicity such as sodium chloride or dextrose. The pH can be adjusted with acids or bases, such as hydrochloric acid or sodium hydroxide. The parenteral preparation can be enclosed in ampoules, disposable syringes or multiple dose vials made of glass or plastic. Pharmaceutically compatible binding agents, and/or adjuvant materials can be included as part of the composition. The tablets, pills, capsules, troches and the like can contain any of the following ingredients, or compounds of a similar nature: a binder such as microcrystalline cellulose, gum tragacanth or gelatin; an excipient such as starch or lactose, a disintegrating agent such as alginic acid, Primogel, or corn starch; a lubricant such as magnesium stearate or Sterotes; a glidant such as colloidal silicon dioxide; a sweetening agent such as sucrose or saccharin; or a flavoring agent such as peppermint, methyl salicylate, or orange flavoring. For administration by inhalation, the compounds are delivered in the form of an aerosol spray from pressured container or dispenser which contains a suitable propellant, e.g., a gas such as carbon dioxide, or a nebulizer. For transmucosal or transdermal administration, penetrants appropriate to the barrier to be permeated are used in the formulation. Such penetrants are generally known in the

art, and include, for example, for transmucosal administration, detergents, bile salts, and fusidic acid derivatives. Transmucosal administration can be accomplished through the use of nasal sprays or suppositories. For transdermal administration, the active compounds are formulated into ointments, salves, gels, or creams as generally
5 known in the art.

Optionally, the formulation will also include a carrier, such as, for example, bovine serum albumin (BSA), keyhole limpet hemocyanin (KLH), ovalbumin, mouse serum albumin, rabbit serum albumin and the like. Means for conjugating peptides to
10 carrier proteins are also well known in the art and include glutaraldehyde, m-maleimidobencoyl-N-hydroxysuccinimide ester, carbodiimide and bis-biazotized benzidine.

In another embodiment, the subject method further comprises producing or
15 synthesizing the compound that is tested on the genetically modified animal.

Peptidyl compounds are conveniently made by standard peptide synthesis, such as the Merrifield method of synthesis (Merrifield, *J Am Chem Soc*, 85:2149-2154, 1963) and the myriad of available improvements on that technology (see e.g.,
20 *Synthetic Peptides: A User's Guide*, Grant, ed. (1992) W.H. Freeman & Co., New York, pp. 382; Jones (1994) *The Chemical Synthesis of Peptides*, Clarendon Press, Oxford, pp. 230.); Barany, G. and Merrifield, R.B. (1979) in *The Peptides* (Gross, E. and Meienhofer, J. eds.), vol. 2, pp. 1-284; Academic Press, New York; Wünsch, E., ed. (1974) *Synthese von Peptiden in Houben-Weyls Methoden der Organischen*
25 *Chemie* (Müller, E., ed.), vol. 15; 4th edn., Parts 1 and 2, Thieme, Stuttgart; Bodanszky, M. (1984) *Principles of Peptide Synthesis*, Springer-Verlag, Heidelberg; Bodanszky, M. & Bodanszky, A. (1984) *The Practice of Peptide Synthesis*, Springer-Verlag, Heidelberg; Bodanszky, M. (1985) *Int. J. Peptide Protein Res.* 25, 449-474.

30 Preferably, the peptide is synthesized on a solid phase support, such as, for example, a polystyrene gel bead comprising polystyrene cross-linked with divinylbenzene, preferably 1% (w.w) divinylbenzene, which is further swollen using lipophilic solvent, such as, for example dichloromethane or dimethylformamide (DMF). The polystyrene can be functionalized by addition of chloromethane or amino methyl

groups. Alternatively, cross-linked and functionalized polydimethyl-acrylamide gel can be used once swollen and solvated using DMF or dipolar aprotic solvent. Other solid phase supports known to those skilled in the art can also be used for peptide synthesis, such as, for example, polyethylene glycol-derived bead produced by
5 grafting polyethylene glycol to the surface of inert polystyrene beads. Preferred commercially available solid phase supports include PAL-PEG-PS, PAC-PEG-PS, KA, KR, or TGR (Applied Biosystems, CA 94404, USA).

For solid phase peptide synthesis, blocking groups that are stable to the
10 repeated treatments necessary for removal of the amino blocking group of the growing peptide chain and for repeated amino acid couplings, are used for protecting the amino acid side-chains during synthesis and for masking undesired reactivity of the α -amino, carboxyl or side chain functional groups. Blocking groups (also called protecting groups or masking groups) thus protect the amino group of the amino acid
15 having an activated carboxyl group that is involved in the coupling reaction, or protect the carboxyl group of the amino acid having an acylated amino group that is involved in the coupling reaction.

During synthesis, coupling occurs following removal of a blocking group without
20 the disruption of a peptide bond, or any protecting group attached to another part of the peptide. Additionally, the peptide-resin anchorage that protects the C-terminus of the peptide is protected throughout the synthetic process until cleavage from the resin is required. Accordingly, by the judicious selection of orthogonally protected α -amino acids, amino acids are added at desired locations to a growing peptide whilst it is still
25 attached to the resin.

Preferred amino blocking groups are easily removable but sufficiently stable to survive conditions for the coupling reaction and other manipulations, such as, for example, modifications to the side-chain groups. In one embodiment, amino blocking
30 groups are selected from the group consisting of: (i) a benzyloxycarbonyl group (Z or carbocenzoxy) that is removed easily by catalytic hydrogenation at room temperature and ordinary pressure, or using sodium in liquid ammonia and hydrobromic acid in acetic acid; (ii) a urethane derivative; (iii) a t-Butoxycarbonyl group (Boc) that is introduced using t-butoxycarbonyl azide or di-tert-butylidicarbonate and removed using

mild acid such as, for example, trifluoroacetic acid (50% TFA in dichloromethane), or HCl in acetic acid/dioxane/ethylacetate; (iv) a 9-fluorenylmethyloxycarbonyl group (Fmoc) that is cleaved under mildly basic, non-hydrolytic conditions, such as, for example, using a primary or secondary amine (eg. 20% piperidine in dimethyl formamide); (v) a 2-(4-biphenyl) propyl(2)oxycarbonyl group (Bpoc); (vi) a 2-nitrophenylsulfenyl group (Nps); and (vii) a dithia-succinyl group (Dts). Boc is widely used to protect the N-terminus in Fmoc chemistry, or Fmoc is widely used to protect the N-terminus in Boc chemistry.

10 Side chain-protecting groups will vary for the functional side chains of the amino acids forming the peptide being synthesized. Side-chain protecting groups are generally based on the Bzl group or the tBu group. Amino acids having alcohols or carboxylic acids in the side-chain are protected as Bzl ethers, Bzl esters, cHex esters, tBu ethers, or tBu esters. Side-chain protection of Fmoc amino acids requires blocking
15 groups that are ideally base stable and weak acid (TFA) labile. Many different protecting groups for peptide synthesis have been described (see *The Peptides*, Gross *et al.* eds., Vol. 3, Academic Press, New York, 1981). For example, the 4-methoxy-2,3,6-trimethylphenylsulfonyl (Nd- Mtr) group is useful for Arginine side-chain protection, however deprotection of Arg(Mtr) requires prolonged TFA treatment. A
20 number of soft acid (TFA, thallium (III) trifluoroacetate/TFA) labile groups, or TFA stable but thallium (III) trifluoroacetate/TFA labile groups, or soft acid stable groups are used to protect Cystine.

The two most widely used protection strategies are the Boc/Bzl- and the
25 Fmoc/tBu-strategies. In Boc/Bzl, Boc is used for amino protection and the side-chains of the various amino acids are protected using Bzl- or cHex-based protecting groups. A Boc group is stable under catalytic hydrogenation conditions and is used orthogonally along with a Z group for protection of many side chain groups. In Fmoc/tBu, Fmoc is used for amino protection and the side-chains are protected with
30 tBu-based protecting groups.

Alternatively, the peptidyl compound is produced by the recombinant expression of nucleic acid encoding the amino acid sequence of said peptide. Random peptide-encoding libraries are particularly preferred for such purposes, because they

provide a wide range of different compounds to test. Alternatively, naturally-occurring nucleic acids can be screened. According to this embodiment, nucleic acid encoding the peptidyl compound is produced by standard oligonucleotide synthesis or derived from a natural source and cloned into a suitable expression vector in operable connection with a promoter or other regulatory sequence capable of regulating expression in a cell-free system or cellular system..

Oligonucleotides are preferably synthesized with linker or adaptor sequences at the 5'- and 3'-ends to facilitate subsequent cloning into a suitable vector system using standard techniques.

Placing a nucleic acid molecule under the regulatory control of, i.e., "in operable connection with", a promoter sequence means positioning said molecule such that expression is controlled by the promoter sequence, generally by positioning the promoter 5' (upstream) of the peptide-encoding sequence.

The prerequisite for producing intact peptides in bacteria such as *E. coli* is the use of a strong promoter with an effective ribosome binding site. Typical promoters suitable for expression in bacterial cells such as *E. coli* include, but are not limited to, the *lacZ* promoter, temperature-sensitive λ_L or λ_R promoters, T7 promoter or the IPTG-inducible *tac* promoter. A number of other vector systems for expressing the nucleic acid molecule of the invention in *E. coli* are well-known in the art and are described, for example, in Ausubel *et al* (*In: Current Protocols in Molecular Biology*, Wiley Interscience, ISBN 047150338, 1987) or Sambrook *et al* (*In: Molecular cloning, A laboratory manual, second edition*, Cold Spring Harbor Laboratory, Cold Spring Harbor, N.Y., 1989). Numerous plasmids with suitable promoter sequences for expression in bacteria and efficient ribosome binding sites have been described, such as for example, pKC30 (λ_L : Shimatake and Rosenberg, *Nature* 292, 128, 1981); pKK173-3 (*tac*: Amann and Brosius, *Gene* 40, 183, 1985), pET-3 (T7: Studier and Moffat, *J. Mol. Biol.* 189, 113, 1986); the pBAD/TOPO or pBAD/Thio-TOPO series of vectors containing an arabinose-inducible promoter (Invitrogen, Carlsbad, CA), the latter of which is designed to also produce fusion proteins with thioredoxin to enhance solubility of the expressed protein; the pFLEX series of expression vectors (Pfizer Inc., CT, USA); or the pQE series of expression vectors (Qiagen, CA), amongst others.

Typical promoters suitable for expression in viruses of eukaryotic cells and eukaryotic cells include the SV40 late promoter, SV40 early promoter and cytomegalovirus (CMV) promoter, CMV-IE (cytomegalovirus immediate early) promoter, H1-RNA promoter, and U6 small nuclear RNA promoter, amongst others. Preferred vectors for expression in mammalian cells (eg., HeLa cells, HUVEC cells, 293 cells, 293 T cells, COS cells, COS-1 cells, CHO cells, CHO.T cells, C2C12 cells, differentiated 3T3-L1 adipocytes, 10T cells) include, but are not limited to, the pcDNA vector suite supplied by Invitrogen, in particular pcDNA 3.1 myc-His-tag comprising the CMV promoter and encoding a C-terminal 6xHis and MYC tag; and the retrovirus vector pSR α tkneo (Muller *et al.*, *Mol. Cell. Biol.*, 11, 1785, 1991). The vector pcDNA 3.1 myc-His (Invitrogen) is particularly preferred for expressing peptides in a secreted form in 293T cells, wherein the expressed peptide or protein can be purified free of conspecific proteins, using standard affinity techniques that employ a Nickel column to bind the protein via the His tag.

A wide range of additional host/vector systems suitable for expressing peptides are available publicly, and described, for example, in Sambrook *et al* (*In: Molecular cloning, A laboratory manual, second edition, Cold Spring Harbor Laboratory, Cold Spring Harbor, N.Y., 1989*).

Means for introducing the nucleic acid or a gene construct comprising same into a cell for expression are well-known to those skilled in the art. The technique used for a given organism depends on the known successful techniques. Means for introducing recombinant DNA into animal cells include microinjection, transfection mediated by DEAE-dextran, transfection mediated by liposomes such as by using lipofectamine (Gibco, MD, USA) and/or cellfectin (Gibco, MD, USA), PEG-mediated DNA uptake, electroporation and microparticle bombardment such as by using DNA-coated tungsten or gold particles (Agracetus Inc., WI, USA) amongst others.

Techniques for synthesizing small organic compounds will vary considerably depending upon the compound, however such methods will be well known to those skilled in the art. In one embodiment, informatics is used to select suitable chemical building blocks from known compounds, for producing a combinatorial library. For

example, QSAR(Quantitative Structure Activity Relationship) modelling approach uses linear regressions or regression trees of compound structures to determine suitability. The software of the Chemical Computing Group, Inc.(Montreal, Canada) uses high-throughput screening experimental data on active as well as inactive compounds, to
5 create a probabilistic QSAR model, which is subsequently used to select lead compounds. The Binary QSAR method is based upon three characteristic properties of compounds that form a "descriptor" of the likelihood that a particular compound will or will not perform a required function: partial charge, molar refractivity (bonding interactions), and logP (lipophilicity of molecule). Each atom has a surface area in the
10 molecule and it has these three properties associated with it. All atoms of a compound having a partial charge in a certain range are determined and the surface areas.(Van der Waals Surface Area descriptor) are summed. The binary QSAR models are then used to make activity models or ADMET models, which are used to build a combinatorial library. Accordingly, information from known appetite suppressants and
15 non-suppressants, including lead compounds identified in initial screens, can be used to expand the list of compounds being screened to thereby identify highly active compounds.

Another embodiment of the invention provides a method of identifying a
20 compound that enhances feeding behavior, such as, for example, in the treatment of anorexia or bulimia, said method comprising: (a) administering a compound that suppresses appetite or dietary intake to a genetically modified non-human animal comprising a genetic modification within an allele of its Cbl locus wherein said genetic modification reduces or prevents expression of a functional endogenous Cbl in said
25 animal and determining the feeding behavior of the animal; (b) administering a compound to the animal and determining the feeding behavior of the animal, wherein enhanced appetite or dietary intake at (b) compared to (a) indicates that the compound enhances feeding behavior.

30 Naturally, the compound administered at (b) will be different to the compound at (a).

Preferably, the compound that suppresses appetite or dietary intake acts via a Cbl-mediated mechanism, which can be verified using the genetically modified Cbl-

deficient animal, such as by determining the ability of the compound to suppress appetite or dietary intake of Cbl-deficient mice according to a method described herein. In this case, step (a) *supra* of administering a compound that suppresses appetite or dietary intake to the genetically modified non-human animal will comprise:

5 (i) administering a compound to a genetically modified non-human animal comprising a genetic modification within an allele of its Cbl locus wherein said genetic modification reduces or prevents expression of a functional endogenous Cbl in said animal; and (ii) determining the feeding behavior of the animal, wherein reduced appetite or dietary intake of the animal compared to a Cbl-deficient animal to which the compound has

10 not been administered indicates that the compound suppresses appetite or dietary intake.

In an alternative embodiment, the invention provides a method of identifying a compound that modulates feeding behavior, such as, for example, in the treatment of

15 anorexia or bulimia, said method comprising: (a) administering a compound to a non-human animal expressing a functional Cbl protein and determining the feeding behavior of the animal; (b) determining the feeding behavior of a genetically modified non-human animal comprising a genetic modification within an allele of its Cbl locus wherein said genetic modification reduces or prevents expression of a functional

20 endogenous Cbl in said animal; and (c) comparing the feeding behavior of the animals at (a) and (b) wherein a comparable feeding behavior between (a) and (b) indicates that the compound modulates feeding behavior.

In one embodiment, the subject method further comprises formulating the

25 identified compound for administration to a non-human animal or a human as described *supra*.

In another embodiment, the subject method further comprises producing or synthesizing the compound that is tested on the genetically modified animal.

30

The compounds contemplated include Cbl inhibitory compounds or antagonists of a biological function of Cbl. In one embodiment, the compound is selected from the group consisting of: a peptide, including a peptide derived from Cbl and capable of inhibiting, reducing or repressing a Cbl function, including binding to a protein selected

from the group consisting of CAP, CrklI and C3G; a Cbl dominant-negative mutant; a non-Cbl peptide inhibitors of Cbl; an antibody or antibody fragment which binds to Cbl and inhibits a Cbl function; a small organic molecule, and nucleic acid, including nucleic acid encoding said peptide derived from Cbl or said non-Cbl peptide inhibitor,
5 an antisense nucleic acid directed against Cbl-encoding mRNA, or an anti-Cbl ribozyme, or a small interfering RNA (RNAi) that targets Cbl gene expression.

The term "antisense nucleic acid" shall be taken to mean DNA or RNA molecule that is complementary to at least a portion of a specific mRNA molecule
10 (Weintraub, Scientific American 262:40, 1990) and capable of interfering with a post-transcriptional event such as mRNA translation. Antisense oligomers complementary to at least about 15 contiguous nucleotides of Cbl-encoding mRNA are preferred, since they are easily synthesized and are less likely to cause problems than larger molecules when introduced into the target Cbl-producing cell. The use of antisense
15 methods is well known in the art (Marcus-Sakura, Anal. Biochem. 172: 289; 1988). Preferred antisense nucleic acid will comprise a nucleotide sequence that is complementary to at least 15 contiguous nucleotides of a sequence encoding the amino acid sequence set forth in SEQ ID NO: 2 or 3.

20 As used herein, a "ribozyme" is a nucleic acid molecule having nuclease activity for a specific nucleic acid sequence. A ribozyme specific for Cbl-encoding mRNA, for example, binds to and cleaves specific regions of the mRNA, thereby rendering it untranslatable. To achieve specificity, preferred ribozymes will comprise a nucleotide sequence that is complementary to at least about 12-15 contiguous
25 nucleotides of a sequence encoding the amino acid sequence set forth in SEQ ID NO: 2 or 3.

As used herein, the terms "small interfering RNA" ("siRNA"), short hairpin RNA ("shRNA"), and "RNAi" refer to homologous double stranded RNA (dsRNA) that
30 specifically targets a gene product, thereby resulting in a null or hypomorphic phenotype. Specifically, the dsRNA comprises two short nucleotide sequences derived from the target RNA encoding Cbl and having self-complementarity such that they can anneal, and interfere with expression of a target gene, presumably at the post-transcriptional level. RNAi molecules are described by Fire et al., Nature 391,

806-811, 1998, and reviewed by Sharp, Genes & Development, 13, 139-141, 1999). As will be known to those skilled in the art, short hairpin RNA ("shRNA") is similar to siRNA, however comprises a single strand of nucleic acid wherein the complementary sequences are separated an intervening hairpin loop such that, following introduction
5 to a cell, it is processed by cleavage of the hairpin loop into siRNA. Accordingly, each and every embodiment described herein is equally applicable to siRNA and shRNA.

Preferred siRNA or shRNA molecules comprise a nucleotide sequence that is identical to about 19-21 contiguous nucleotides of the target mRNA. Preferably, the
10 target sequence in Cbl mRNA commences with the dinucleotide AA, comprises a GC-content of about 30-70% (preferably, 30-60%, more preferably 40-60% and more preferably about 45%-55%), and does not have a high percentage identity to any nucleotide sequence other than a c-Cbl protooncogene in the genome of the animal in which it is to be introduced, e.g., as determined by standard BLAST search.

15

The siRNA or shRNA is preferably capable of downregulating expression of human c-Cbl in a cell. In view of the high percentage conservation between murine and human c-Cbl-encoding genes, especially in the coding regions, this should not be taken to indicate a requirement for the siRNA or shRNA to be specific for human c-
20 Cbl-encoding genes. In the cell-based and animal models described herein, it is possible and appropriate in certain circumstances for the siRNA or shRNA molecules to reduce expression of both endogenous murine c-Cbl, as well as ectopically expressed human c-Cbl in the cell. Confirmation of a specific activity of any antagonist against human c-Cbl is determined by assessing the activity of an inhibitor in a cell
25 derived from a c-Cbl^{-/-} mouse that has been engineered to express human c-Cbl.

As exemplified herein, preferred siRNA against a c-Cbl encoding gene comprises a 21-nucleotide sequence set forth in any one of SEQ ID Nos: 4-239. In this respect, SEQ ID Nos: 4-121 each comprise (i) a 19-nucleotide sequence
30 corresponding to a human c-Cbl mRNA target sequence adjacent and downstream of a dinucleotide AA in said mRNA target; and (ii) a 3'-extension dinucleotide TT. SEQ ID NOS: 122-239 each comprise (i) a 19-nucleotide sequence complementary to a human c-Cbl mRNA target sequence contained within SEQ ID NOS: 4-121, respectively; and (ii) a 3'-extension dinucleotide TT.

For producing shRNA from the exemplified siRNAs set forth in SEQ ID NOS: 4-239, the sense and antisense strands are positioned such that they flank an intervening loop sequence. Preferred loop sequences are selected from the group consisting of:

- (i) CCC (SEQ ID NO: 240);
- (ii) TTCG (SEQ ID NO: 241);
- (iii) CCACC (SEQ ID NO: 242);
- (iv) CTCGAG (SEQ ID NO: 243);
- (v) AAGCTT (SEQ ID NO: 244);
- (vi) CCACACC (SEQ ID NO: 245); and
- (vii) TTCAAGAGA (SEQ ID NO: 246).

Of these loop sequences, the sequence set forth in SEQ ID NO: 246 is particularly preferred for modulating human c-Cbl expression in a cell, tissue (eg., skeletal muscle, or whole organism).

Preferred siRNA molecules that are selectively active against human c-Cbl expression compared to murine c-Cbl expression are derived from the sequence of the 5'-non-coding and/or 3'-non-coding region of the human c-Cbl gene. Such specific siRNAs include, e.g., SEQ ID Nos: 57-59, 117-121, 175-177 and 235-239.

The antisense RNA, ribozyme, siRNA or shRNA can be introduced directly to a cell or cell-free extract capable of expressing c-Cbl as naked DNA. Alternatively, DNA encoding a nucleic acid inhibitory molecule can be introduced into a cell in operable connection with a suitable promoter and transcription terminator sequence to facilitate expression of the inhibitory nucleic acid. Preferred promoters for expression in mammalian cells that express Cbl include the CMV promoter, ubiquitin promoter, U6 small nuclear RNA promoter (Lee *et al.*, *Nature Biotech.* 20, 500-505, 2002; Miyagishi *et al.*, *Nature Biotech.* 20, 497-500, 2002; Paul *et al.*, *Nature Biotech.* 20, 505-508, 2002; and Yu *et al.*, *Proc. Natl Acad. Sci USA* 99, 6047-6052, 2002), H1-RNA promoter (Brummelkamp *et al.*, *Science* 296, 550-553, 2002), or other RNA polymerase III promoter. The pol III terminator is also preferred for such applications. Other promoters and terminators are not to be excluded.

In one embodiment, the DNA encoding the inhibitory nucleic acid is operably connected to promoter and terminator regulatory sequences by cloning into a suitable vector that comprises the necessary promoter and transcriptional terminator sequences, and the recombinant vector is then introduced to the cell, tissue or organ by transient transfection of plasmid DNA, by establishing permanent cell lines or in infection with retroviral expression vectors (Barton *et al.*, *Proc. Natl Acad. Sci USA* 99, 14943-14945, 2002; Devroe *et al.*, *BMC Biotech.* 2, p15, 2002).

In high throughput primary assays at least, it is preferred to use an *in vitro* cell-free system or cell-based system in which Cbl activity is assayed. Several vectors are known for this purpose, including, for example, the pSilencer series of vectors (pSilencer 2.0, pSilencer 2.1, pSilencer 3.0, pSilencer 3.1, pSilencer 1.0-U6) provided by Ambion.

Preferred retroviral vectors, suitable for transiently transfecting into isolated cells e.g., by calcium phosphate precipitation (Ketteler *et al.*, *Gene Ther.* 9, 477-487, 2002) in high throughput screens, or for the production of transducing supernatants (Ketteler *et al.*, *Gene Ther.* 9, 477-487, 2002) for lower-throughput screening or validation of primary screen results, include pBabe (Morgenstern *et al.*, *Nuc. Acids Res.* 18, 3587-3596, 1990) and JZenNeo.

The pBabe retroviral vector constructs transmit inserted genes at high titres and express them from the Mo MuLV Long Terminal Repeat (LTR). The pBabe vectors comprise one of four different dominantly-acting selectable markers, allowing the growth of infected mammalian cells in the presence of G418, hygromycin B, bleomycin/phleomycin or puromycin. The high titre ecotropic helper free packaging cell line, omega E, reduces the risk of generation of wild type Mo MuLV via homologous recombination events. Together, the pBabe vectors and omega E cell line provide high frequency gene transfer, and/or concomitant expression of c-Cbl with one or more other genes (e.g., APS and/or Insulin receptor β -subunit) in a single cell, with minimal risk of helper virus contamination.

For lower throughput primary screening or validation assays, the adenoviral vectors pAdTrack and pAdTrack-CMV (He *et al.*, *Proc. Natl Acad. Sci USA* 95, 2509-

2514, 1998; pAdTrack-HP (Zhao *et al.*, *Gene* 316, 137-141, 2003), an Ad5CMV-based vector e.g., Ad5CMV-GFP (Suoka *et al.*, *Am. J. Respir. Cell Mol. Biol.* 23, 297-303, 2000), and pSilencer adeno 1.0-CMV (Ambion) are preferred for delivery and expression in specific organs or tissues, in particular muscle tissue of a mouse model.

5

The pAdTrack and pAdTrack-CMV vectors are particularly preferred for applications which require standardization for transfection or transduction efficiency eg., injection of adenovirus into hindlimb muscles of transgenic mouse models. The pAdTrack vector is used for production of GFP-trackable viruses containing
10 transgenes under the control of a chosen promoter. It contains the gene encoding enhanced GFP, a polylinker for insertion of exogenous transgenes surrounded by adenoviral sequences ("arms") that allow homologous recombination with pAdEasy-1. The left arm contains Ad5 nucleotides 34,931-35,935, which mediate homologous recombination with pAdEasy vectors in *E. coli*, plus inverted terminal repeat (ITR) and
15 packaging signal sequences (nucleotides 1-480 of Ad5) required for viral production in mammalian cells. The right arm contains Ad5 nucleotides 3,534-5,790, which mediate homologous recombination with pAdEasy vectors. Artificially created *PacI* sites surround both arms. The AdTrack plasmid also contains a kanamycin resistance gene from pZero 2.1 (Invitrogen) and the origin of replication from pBR322 (Life
20 Technologies). The relatively low copy number of plasmids generated with this origin is essential for the stability of large constructs in *E. coli*. The pAdTrack-CMV vector is identical to pAdTrack except for the addition of a cytomegalovirus (CMV) promoter and polyadenylation site (both from pEGFP-C1, Clontech). A polylinker is present between the CMV promoter and polyadenylation site.

25

As will be known to the skilled artisan, such adenoviral vectors are also suitable for transfection of cell lines.

The term "dominant-negative mutant" refers to a Cbl polypeptide that has been
30 mutated from its natural state and that interacts with a protein that Cbl normally interacts with thereby preventing endogenous native Cbl from forming the interaction. Preferred dominant negative mutants will lack that portion of Cbl that interacts with a protein selected from the group consisting of CAP, Crkl and C3G.

Preferred dominant-negative mutants comprise variants of the native Cbl protein, such as, for example, substitution or deletion mutants, that act as dominant-negative mutants of Cbl function. For example, a dominant-negative mutant may comprise one or more amino acid substitutions within the RING domain of c-Cbl.

5 When expressed in a cell, such a dominant-negative mutant protein competes with native endogenous c-Cbl for the APS protein and/or insulin receptor β -subunit, however has reduced or no E3 ubiquitin ligase activity with respect to the receptor. In an alternative embodiment, the dominant-negative mutant comprises 1 or 2 or 3 substitutions of tyrosine residues that would normally be phosphorylated in the cell.

10 Means for producing mutated nucleic acid are well known to those skilled in the art and may be achieved readily e.g., using the Quick Change Mutagenesis kit supplied by Stratagene, La Jolla, California USA according to the manufacturer's instructions.

Dominant negative mutant proteins are produced by expression of nucleic acid encoding the mutant protein, essentially as described herein above for expression of

15 peptides in cells. The amino acid sequences of exemplary dominant-negative mutants of c-Cbl are set forth in SEQ ID NO: 248 (c-Cbl G306E), SEQ ID NO: 250 (c-Cbl C381A), SEQ ID NO: 252 (c-Cbl Y700F), SEQ ID NO: 254 (c-Cbl Y731F), SEQ ID NO: 256 (c-Cbl Y774F), SEQ ID NO: 258 (c-Cbl Y700F/Y731F/Y774F) and SEQ ID NO:

20 260 (c-Cbl480 i.e, truncated at residue 480 of native human c-Cbl).

The "antibodies" contemplated herein are immunoreactive with Cbl polypeptides or functional fragments thereof. Antibodies that consist essentially of pooled monoclonal antibodies with different epitope specificities, as well as distinct

25 monoclonal antibody preparations are contemplated. Monoclonal antibodies are produced from fragments of the Cbl protein that comprise one or more B cell epitopes by methods well known to those skilled in the art (Kohler et al, Nature 256:495, 1975). The term "antibody" as used herein includes intact molecules as well as fragments thereof, such as Fab and F(ab')₂, Fv and single chain antibody fragments capable of

30 binding an epitopic determinant of Cbl.

An "Fab fragment" consists of a monovalent antigen-binding fragment of an antibody molecule, and can be produced by digestion of a whole antibody molecule

with the enzyme papain, to yield a fragment consisting of an intact light chain and a portion of a heavy chain.

An "Fab' fragment" of an antibody molecule can be obtained by treating a whole antibody molecule with pepsin, followed by reduction, to yield a molecule consisting of an intact light chain and a portion of a heavy chain. Two Fab' fragments are obtained per antibody molecule treated in this manner.

An "F(ab')₂ fragment" of an antibody consists of a dimer of two Fab' fragments held together by two disulfide bonds, and is obtained by treating a whole antibody molecule with the enzyme pepsin, without subsequent reduction. A (Fab').sub.2 fragment.

An "Fv fragment" is a genetically engineered fragment containing the variable region of a light chain and the variable region of a heavy chain expressed as two chains.

A "single chain antibody" (SCA) is a genetically engineered single chain molecule containing the variable region of a light chain and the variable region of a heavy chain, linked by a suitable, flexible polypeptide linker.

In one embodiment, peptidyl Cbl inhibitors are chemically or recombinantly synthesized as oligopeptides (approximately 10-25 amino acids in length) spanning the Cbl sequence (SEQ ID NO: 2 or 3). Alternatively, Cbl fragments are produced by digestion of native or recombinantly produced Cbl by, for example, using a protease, e.g., trypsin, thermolysin, chymotrypsin, or pepsin. Computer analysis (using commercially available software, e.g. MacVector, Omega, PCGene, Molecular Simulation, Inc.) is used to identify proteolytic cleavage sites. The proteolytic or synthetic fragments can comprise as many amino acid residues as are necessary to partially or completely inhibit Cbl function. Preferred fragments will comprise at least 5, 10, 15, 20, 25, 30, 35, 40, 45, 50, 55, 60, 65, 70, 75, 80, 85, 90, 95, 100 or more amino acids in length.

In one embodiment, peptides are selected which contain a sufficient number of B cell epitopes to elicit antibodies when administered to a mammal. Such peptides are identified by immunizing a mammal with the peptide alone, or in combination with an adjuvant, or linked to an adjuvant (e.g., a hapten). Sera from the immunized animal
5 are tested for anti-Cbl antibodies. Preferred peptides generate anti-Cbl antibodies that inhibit a Cbl function.

Preferred peptidyl Cbl inhibitors will also not comprise a sufficient number of T cell epitopes to induce T-cell mediated (e.g., cytokine) responses when determined
10 using any of a number of well known techniques, such as epitope prediction using algorithms (see e.g., Rothbard and Taylor EMBO J. 7: 93-100, 1988; Berzofsky, Philos Trans R. Soc. Lond. 323: 535-544, 1989; Rothbard, 1st Forum in Virology, Annals of the Pasteur Institute, pp 518-526, Dec. 1986; Rothbard and Taylor, Embo, 7: 93-100, 1988; EP 0 304 279; and Margalit et al., J. Immunol., 138: 2213-2229, 1987); or
15 screening of peptide inhibitors for human T cell stimulating activity or T cell proliferation assays (e.g. Proc. Natl. Acad. Sci USA, 86:1333, 1989).

Other preferred peptide inhibitors of Cbl are located on the surface of the Cbl proteins, e.g., hydrophilic regions, as well as regions with high antigenicity or
20 fragments with high surface probability scores can be identified using computer analysis programs well known to those of skill in the art (Hopp and Wood, (1983), Mol. Immunol., 20, 483-9, Kyte and Doolittle, (1982), J. Mol. Biol., 157, 105-32, Corrigan and Huang, (1982), Comput. Programs Biomed, 3, 163-8).

25 Anti-Cbl antibodies or antibody fragments are generated using the entire Cbl polypeptide or an immunogenic fragment thereof (alone or linked to a suitable carrier or hapten) to immunize a subject (e.g., a mammal including, but not limited to a rabbit, goat, mouse or other mammal). For example, the methods described in U.S. Pat. Nos. 5,422,110; 5,837,268; 5,708,155; 5,723,129; and 5,849,531, can be used and are
30 incorporated herein by reference. In a preferred embodiment, the mammal being immunized does not contain endogenous Cbl (e.g., a Cbl-deficient genetically modified animal). The immunogenic preparation can further include an adjuvant, such as Freund's complete or incomplete adjuvant, or similar immunostimulatory agent. Immunization of a suitable subject with an immunogenic proteolytic or synthetic Cbl

peptide preparation induces a polyclonal anti-Cbl antibody response. The anti-Cbl antibody titer in the immunized subject is generally monitored over time by standard techniques, such as with an enzyme linked immunosorbent assay (ELISA) using immobilized Cbl. Subsequently, the sera from the immunized subjects can be tested
5 for Cbl inhibitory activity.

Alternatively, it is also possible to immunize the subject with nucleic acid expressing Cbl using DNA immunization technology, such as that disclosed in U.S. Pat. No. 5,795,872 to Ricigliano et al., or alternatively, in U.S. Pat. No. 5,643,578 to
10 Robinson et al.

The antibody molecules directed against Cbl can be isolated from the mammal (e.g., from the blood) and further purified by well known techniques, such as protein A chromatography to obtain the IgG fraction. At an appropriate time after immunization,
15 e.g., when the anti-Cbl antibody titers are highest, antibody-producing cells can be obtained from the subject and used to prepare e.g., monoclonal antibodies by standard techniques, such as the hybridoma technique originally described in the following disclosures: Kohler and Milstein Nature 256:495-497, 1975; Brown et al. J. Immunol. 127:53946, 1981; Brown et al. J. Biol Chem. 255: 4980-4983, 1980; Yeh et
20 al. Proc. Natl. Acad. Sci. USA 76:2927-2931, 1976; Yeh et al. Int. J. Cancer 29: 269-275, 1982; Kozbor et al. Immunol Today 4:72, 1983; Cole et al., Monoclonal Antibodies and Cancer Therapy, Alan R. Liss, Inc., pp. 77-96, 1985. The technology for producing monoclonal antibody hybridomas is well known in the art. Briefly, an immortal cell line (typically a myeloma) is fused to lymphocytes (typically splenocytes)
25 from a mammal immunized with a Cbl peptide immunogen as described above, and the culture supernatants of the resulting hybridoma cells are screened to identify a hybridoma producing a monoclonal antibody that binds Cbl.

Any of the known protocols used for fusing lymphocytes and immortalized cell
30 lines can be applied for the purpose of generating an anti-Cbl monoclonal antibody (see, e.g., G. Galfre et al., Nature-266: 550-552, 1970). Moreover, the ordinarily skilled worker will appreciate that there are many variations of such methods which also would be useful. Typically, the immortal cell line (e.g., a myeloma cell line) is derived from the same mammalian species as the lymphocytes. For example, murine

hybridomas can be made by fusing lymphocytes from a mouse immunized with an immunogenic preparation of the present invention with an immortalized mouse cell line. Preferred immortal cell lines are mouse myeloma cell lines that are sensitive to culture medium containing hypoxanthine, aminopterin and thymidine ("HAT medium").

5 Any of a number of myeloma cell lines can be used as a fusion partner according to standard techniques, e.g., the P3-NS1/1-Ag4-1, P3-x63-Ag8.653 or Sp2/O-Ag14 myeloma lines. These myeloma lines are available from ATCC. Typically, HAT-sensitive mouse myeloma cells are fused to mouse splenocytes using polyethylene glycol ("PEG"). Hybridoma cells resulting from the fusion are then selected using HAT

10 medium, which kills unfused and unproductively fused myeloma cells (unfused splenocytes die after several days because they are not transformed). Hybridoma cells producing a monoclonal antibody of the invention are detected by screening the hybridoma culture supernatants for antibodies that bind Cbl, e.g., using a standard ELISA assay. The antibodies can then be tested for Cbl inhibitory activity.

15 In one embodiment, the present invention a small organic molecule inhibitor or antagonist of c-Cbl is a compound that reduces the E3 ubiquitin ligase activity of c-Cbl thereby reduces the ubiquitination of the insulin receptor β -subunit by c-Cbl. Preferably, the small organic molecule is a non-competitive inhibitor of c-Cbl with

20 respect to ubiquitin and the insulin receptor β -subunit. In a preferred embodiment, the small organic molecule belongs to a class of compounds that binds to the RING finger domain of c-Cbl (i.e. an amino acid sequence comprising or contained within residues from about position 380 to about position 421 of SEQ ID NO: 3), e.g., a benzsulfonamide, urea, or imidazolone.

25 A further aspect of the present invention provides a method of identifying a compound that enhances fat deposition or reduces lean muscle mass or enhances the ratio of body fat to muscle or reduces metabolic rate, such as, for example, in the treatment of hypolipidemia (e.g. as observed in subjects suffering from

30 abetalipoproteinemia, malnutrition or hematologic malignancies, such as acute myelocytic leukemia or chronic myelocytic leukemia), said method comprising: (a) administering a compound to a genetically modified non-human animal comprising a genetic modification within an allele of its Cbl locus wherein said genetic modification reduces or prevents expression of a functional endogenous Cbl in said animal; and (b)

determining the fat content of the animal, wherein enhanced fat content of the animal compared to the fat content of a Cbl-deficient animal to which the compound has not been administered indicates that the compound enhances fat deposition or reduces lean muscle mass or enhances the ratio of body fat to muscle or reduces metabolic rate.

By "fat deposition" is meant the amount of fat deposited or the rate at which fat is deposited in liver, fat or muscle cells. Standard means known to the skilled artisan are used to determine fat deposition. "Lean muscle mass" means muscle tissue that is substantially fat-free. The "ratio of body fat to muscle mass" means the relative amount of total body fat to total non-fat tissue. "Metabolic rate" means the ability of a subject to utilize dietary intake for immediate energy needs, rather than store such dietary intake as body fat.

The genetically modified animal and the Cbl-deficient animal are described *supra*.

The range of compounds contemplated herein for enhancing fat deposition or reducing lean muscle mass or enhancing the ratio of body fat to muscle or reducing metabolic rate include peptides, including peptides derived from Cbl and capable of complementing the Cbl-deficiency; non-Cbl peptides, such as, for example Cbl peptidomimetics; small organic molecules, such as, for example derived from publicly available combinatorial libraries; and nucleic acids, including nucleic acid encoding said peptide derived from Cbl or said non-Cbl peptide. Such compounds are described *supra*.

In one embodiment, the subject method further comprises formulating the identified compound for administration to a non-human animal or a human. Such formulations are described *supra*.

In another embodiment, the subject method further comprises producing or synthesizing the compound that is tested on the genetically modified animal. Such methods are described *supra*.

In an alternative embodiment, the invention provides a method of identifying a compound that reduces fat deposition or enhances lean muscle mass or reduces the ratio of body fat to muscle or enhances metabolic rate, such as, for example, in the treatment of obesity, said method comprising: (a) administering a compound that
5 enhances fat deposition or glucose uptake to a genetically modified non-human animal comprising a genetic modification within an allele of its Cbl locus wherein said genetic modification reduces or prevents expression of a functional endogenous Cbl in said animal and determining the fat content of the animal; (b) administering a compound to
10 the animal and determining the fat content of the animal, wherein a similar or reduced fat content at (b) compared to (a) indicates that the compound reduces fat deposition or enhances lean muscle mass or reduces the ratio of body fat to muscle or enhances
metabolic rate.

Preferably, the animal is maintained on a diet comprising high glycemic index
15 food, such as, for example, carrots or food supplemented with sucrose.

Preferably, the compound that enhances fat deposition, or reduces lean muscle mass or enhances the ratio of body fat to muscle or reduces metabolic rate acts via a Cbl-mediated mechanism, which can be verified using the genetically
20 modified Cbl-deficient animal, such as by determining the ability of the compound to enhance fat content of Cbl-deficient mice according to a method described herein. In this case, step (a) *supra* of administering a compound that enhances fat deposition or glucose uptake comprises (i) administering a compound to a genetically modified non-
human animal comprising a genetic modification within an allele of its Cbl locus
25 wherein said genetic modification reduces or prevents expression of a functional endogenous Cbl in said animal; and (ii) determining the fat content of the animal, wherein enhanced fat content of the animal compared to a Cbl-deficient animal to which the compound has not been administered indicates that the compound
enhances fat deposition, or reduces lean muscle mass or enhances the ratio of body
30 fat to muscle or reduces metabolic rate.

In an alternative embodiment, the invention provides a method of identifying a compound that reduces fat deposition or enhances lean muscle mass or reduces the ratio of body fat to muscle or enhances metabolic rate comprising: (a) administering a

compound to a non-human animal expressing a functional Cbl protein and determining the fat content of the animal; (b) determining the fat content of a genetically modified non-human animal comprising a genetic modification within an allele of its Cbl locus wherein said genetic modification reduces or prevents expression of a functional
5 endogenous Cbl in said animal; and (c) comparing the fat contents of the animals at (a) and (b) wherein a comparable fat content between (a) and (b) indicates that the compound reduces fat deposition or enhances lean muscle mass or reduces the ratio of body fat to muscle or enhances metabolic rate.

10 Preferably, the animals are maintained on similar or identical diets, more preferably, on diets comprising high glycemic index food.

The compounds contemplated herein include Cbl inhibitory compounds or antagonists of a biological function of Cbl. In one embodiment, the compound is
15 selected from the group consisting of: a peptide, including a peptide derived from Cbl and capable of inhibiting, reducing or repressing a Cbl function, including binding to a protein selected from the group consisting of CAP, CrklI and C3G; a Cbl dominant-negative mutant; a non-Cbl peptide inhibitors of Cbl; an antibody or antibody fragment which binds to Cbl and inhibits a Cbl function; a small organic molecule, and nucleic
20 acid; including nucleic acid encoding said peptide derived from Cbl or said non-Cbl peptide inhibitor, an antisense nucleic acid directed against Cbl-encoding mRNA, an anti-Cbl ribozyme, RNAi or siRNA.

In one embodiment, the subject method further comprises formulating the
25 identified compound for administration to a non-human animal or a human. Such formulations are described *supra*.

In another embodiment, the subject method further comprises producing or synthesizing the compound that is tested on the genetically modified animal. Such
30 methods are described *supra*.

A further aspect of the present invention provides a method of identifying a compound that enhances glucose uptake such as, for example, in the treatment of hypolipidemia (e.g. as observed in subjects suffering from abetalipoproteinemia,

malnutrition or hematologic malignancies, such as acute myelocytic leukemia or chronic myelocytic leukemia), said method comprising: (a) administering a compound to a genetically modified non-human animal comprising a genetic modification within an allele of its Cbl locus wherein said genetic modification reduces or prevents
5 expression of a functional endogenous Cbl in said animal; and (b) determining the glucose uptake into liver, fat or muscle cells of the animal, wherein enhanced uptake compared to the glucose uptake into liver, fat or muscle cells of a Cbl-deficient animal to which the compound has not been administered indicates that the compound enhances glucose uptake.

10

Means for determining glucose uptake are well known in the art. Preferably, the process is performed *ex vivo* using liver, fat or muscle cells that have been previously isolated from the animal. In one embodiment, the glucose uptake is basal glucose uptake (i.e. glucose uptake measured in the absence of exogenously
15 administered insulin). In another embodiment, the glucose uptake is insulin-mediated glucose uptake (i.e. glucose uptake measured following administration of insulin). All embodiments of the invention described herein apply *mutatis mutandis* to both basal glucose uptake and insulin-mediated glucose uptake unless otherwise stated.

20

The genetically modified animal and the Cbl-deficient animal are described *supra*.

The range of compounds contemplated herein for enhancing glucose uptake include peptides, including peptides derived from Cbl and capable of complementing
25 the Cbl-deficiency; non-Cbl peptides, such as, for example Cbl peptidomimetics; small organic molecules, such as, for example derived from publicly available combinatorial libraries; and nucleic acids, including nucleic acid encoding said peptide derived from Cbl or said non-Cbl peptide. Such compounds are described *supra*.

30

In one embodiment, the subject method further comprises formulating the identified compound for administration to a non-human animal or a human. Such formulations are described *supra*.

In another embodiment, the subject method further comprises producing or synthesizing the compound that is tested on the genetically modified animal. Such methods are described *supra*.

5 In an alternative embodiment, the invention provides a method of identifying a compound that reduces glucose uptake into liver, fat or muscle cells, such as, for example, in the treatment of obesity, said method comprising: (a) administering a compound that enhances glucose uptake to a genetically modified non-human animal comprising a genetic modification within an allele of its Cbl locus wherein said genetic
10 modification reduces or prevents expression of a functional endogenous Cbl in said animal and determining the glucose uptake into liver, fat or muscle cells; (b) administering a compound to the animal and determining the glucose uptake into liver, fat or muscle cells of the animal, wherein a similar or reduced uptake at (b) compared to (a) indicates that the compound reduces glucose uptake into liver, fat or muscle
15 cells.

Preferably, the animal is maintained on a diet comprising high glycemic index food, such as, for example, carrots or food supplemented with sucrose.

20 Preferably, the compound that enhances glucose uptake into liver, fat or muscle cells acts via a Cbl-mediated mechanism, which can be verified using the genetically modified Cbl-deficient animal, such as by determining the ability of the compound to enhance glucose uptake into liver, fat or muscle cells of Cbl-deficient mice according to a method described herein. In this case, step (a) *supra* of
25 administering a compound that enhances glucose uptake into liver, fat or muscle cells comprises (i) administering a compound to a genetically modified non-human animal comprising a genetic modification within an allele of its Cbl locus wherein said genetic modification reduces or prevents expression of a functional endogenous Cbl in said animal; and (ii) determining the glucose uptake into liver, fat or muscle cells of the
30 animal, wherein enhanced glucose uptake into liver, fat or muscle cells of the animal compared to a Cbl-deficient animal to which the compound has not been administered indicates that the compound enhances glucose uptake into liver, fat or muscle cells.

In an alternative embodiment, the invention provides a method of identifying a compound that reduces glucose uptake into liver, fat or muscle cells comprising: (a) administering a compound to a non-human animal expressing a functional Cbl protein and determining the glucose uptake into liver, fat or muscle cells of the animal; (b) 5 determining the glucose uptake into liver, fat or muscle cells of a genetically modified non-human animal comprising a genetic modification within an allele of its Cbl locus wherein said genetic modification reduces or prevents expression of a functional endogenous Cbl in said animal; and (c) comparing the glucose uptake into liver, fat or muscle cells of the animals at (a) and (b) wherein a comparable uptake between (a) 10 and (b) indicates that the compound reduces glucose uptake into liver, fat or muscle cells.

Preferably, the animals are maintained on similar or identical diets, more preferably, on diets comprising high glycemic index food.

15

The compounds contemplated herein include Cbl inhibitory compounds or antagonists of a biological function of Cbl. In one embodiment, the compound is selected from the group consisting of: a peptide, including a peptide derived from Cbl and capable of inhibiting, reducing or repressing a Cbl function, including binding to a 20 protein selected from the group consisting of CAP, CrklI and C3G; a Cbl dominant-negative mutant; a non-Cbl peptide inhibitors of Cbl; an antibody or antibody fragment which binds to Cbl and inhibits a Cbl function; a small organic molecule, and nucleic acid, including nucleic acid encoding said peptide derived from Cbl or said non-Cbl peptide inhibitor, an antisense nucleic acid directed against Cbl-encoding mRNA, or an 25 anti-Cbl ribozyme.

In one embodiment, the subject method further comprises formulating the identified compound for administration to a non-human animal or a human. Such formulations are described *supra*.

30

In another embodiment, the subject method further comprises producing or synthesizing the compound that is tested on the genetically modified animal. Such methods are described *supra*.

In an alternative embodiment, the screening assays supra are performed in vitro using a format that determines the E3 ubiquitin ligase activity of Cbl. Such assays are based upon the knowledge that the APS adapter protein couples the precursor insulin receptor β -subunit to the phosphorylation of c-Cbl and facilitates ligand-stimulated ubiquitination of the insulin receptor (IR- β) (Ahmed *et al.*, *FEBS Letts* 475, 31-34, 2000). Accordingly, to determine ubiquitination of the insulin receptor by c-Cbl, cells that either express APS, c-Cbl and IR- β are required. CHO.T cells are particularly preferred for this purpose, because they are known to over express the IR- β precursor protein.

10

In one embodiment, a test sample is contacted with a test compound under suitable test conditions, wherein the test sample comprises APS protein, c-Cbl protein, insulin receptor (IR- β) protein, an E1 enzyme, a ubiquitin conjugating enzyme, ubiquitin and adenosine 5'-triphosphate (ATP). The ubiquitination of IR- β is determined and the level of ubiquitination of IR- β in the test sample with the ubiquitination of IR- β incubated under the same test conditions in the absence of test compound is determined. The level of ubiquitination of IR- β in the test sample is indicative of the ability of the test compound to modulate ubiquitin ligase activity of c-Cbl. An increase in the level of ubiquitination is an indication that ubiquitin ligase activity of c-Cbl has been enhanced, whereas a decrease in the level of ubiquitination is an indication that ubiquitin ligase activity of c-Cbl has been inhibited.

E1 enzyme is well known to one of skill in the art (e.g., Hershko *et al.*, *Ann. Rev. Biochem.* 61:761-807, 1992; and Monia *et al.*, *Biotechnol.* 8: 209-215, 1990, herein incorporated by reference). E1 enzyme initiates the ubiquitination process by activating ubiquitin. Any of the E1 enzymes known in the art are suitable for use.

Ubiquitin conjugating enzymes transfer ubiquitin to lysine residues of suitable substrates. They also undergo auto-ubiquitination. Suitable ubiquitin conjugating enzymes that can be employed in the invention method include Cdc34, Ubch1, Ubch2, Ubch3, Ubch4, Ubch5, Ubch6, Ubch7, Ubch10, L-UBC, and the like (see Kaiser, *et al.*, *FEBS Letts* 350:1-4, 1994; Kaiser, *et al.*, *FEBS Letts* 377:193-196, 1995; Nuber, *et al.*, *J Biol Chem* 271:2795-2800, 1996; Jensen, *et al.*, *J Biol Chem* 270:30408-30414, 1995; Robinson, *et al.*, *Mamm Genome* 6:725-731, 1995; and Plon

et al., Proc. Natl. Acad. Sci. USA 90:10484-10488, all of which are herein incorporated by reference). "Cdc34" refers to a ubiquitin-conjugating enzyme isolated from yeast.

In one embodiment, the ubiquitin is a derivatized ubiquitin conjugated to a label
5 that is readily identified. For example, the derivatized ubiquitin can be [¹²⁵I]-ubiquitin, a fluorescent ubiquitin, a glutathione S-transferase conjugated ubiquitin or a biotinylated ubiquitin. Using assays well known in the art, the presence of the label, and thus the amount of derivatized ubiquitination, can be identified.

10 Ubiquitination results in an increase in the molecular weight of the IR- β polypeptide. Accordingly, any assay that determines the molecular weight of the IR- β polypeptide, such as, for example, SDS-polyacrylamide gel electrophoresis, mass spectrometry or a variant thereof (MALDI, MALDI-TOF, MS/MS, etc), can be used to measure ubiquitination. High throughput procedures, such as, for example, MS/MS
15 and MALDI-TOF are particularly preferred.

The ubiquitination assay is readily adapted to the large scale screening of compound libraries by converting it to a solid phase format. In one specific non-limiting example, ubiquitination assays can be performed with an appropriately engineered
20 chimeric IR- β protein immobilized on a microtiter plate, in the presence of a derivatized ubiquitin. A "chimeric IR- β protein" in this context is an IR- β precursor polypeptide comprising a heterologous peptide or polypeptide. Preferred heterologous peptides in this context include a myc epitope-hexahistidine tag positioned at the C-terminus of IR- β (i.e., IR- β -myc-His₆).

25

In one embodiment of high throughput screening for ubiquitination of IR- β , components of the reaction mixture are contacted, and aliquots of the ubiquitination assays are transferred to a microtiter plate with an appropriate surface to permit binding of IR- β protein thereto. Preferably, reactions are transferred to a microtiter
30 plate whose wells have been coated with anti- IR- β antibody or anti-myc antibody. After washing away unbound proteins, the substrate-coated wells are directly imaged (e.g., for reactions performed with fluorescent or radio-labeled ubiquitin). The assay may be conducted in replica plates e.g., in the presence or absence of a series of compounds being tested.

In an alternative embodiment, ubiquitination of the IR- β substrate in the presence of a compound is determined using a cell-based assay. The only requirement for such an assay is that the compound being tested is capable of entering the cell. Accordingly, such an assay is particularly useful for identifying peptidyl and nucleic acid modulatory compounds that can be efficiently expressed following transfection or transduction into cells e.g., ribozymes, antisense, siRNA, shRNA, dominant negative modulatory. Such assays may also be amenable for determining the efficacy of antibodies or small organic molecules. This embodiment is based upon the finding that detectable c-Cbl-mediated ubiquitination of IR- β precursor occurs in CHO.T cells expressing myc-tagged APS (Ahmed *et al.*, *FEBS Letts* 475, 31-34, 2000).

In one embodiment, cells capable of expressing APS, c-Cbl and IR- β precursor are incubated in the presence ubiquitin or a derivatized ubiquitin and a chemical compound to be tested for a time and under conditions sufficient for c-Cbl-mediated ubiquitination of IR- β precursor to occur, and the amount of ubiquitin bound to the IR- β precursor is determined.

In contrast to the cell-free system described *supra*, specific detection of ubiquitinated IR- β precursor is required, because other proteins will be ubiquitinated in the cells. Accordingly, it is particularly preferred to determine the amount of ubiquitin bound to IR- β precursor by first capturing the insulin receptor holoprotein or IR- β precursor polypeptide with an antibody (e.g., anti-insulin receptor antibody 83-14, Abcam, Inc, Cambridge MA 02139, USA; or specific anti- IR- β antibody as supplied e.g., by Lab Vision Corp., Fremont CA 94539, USA) and then detecting the amount of ubiquitin bound thereto using a second antibody that specifically binds ubiquitin (Santa Cruz Biotechnology, Santa Cruz, CA, USA). As with the cell-free assay system *supra*, a derivatized ubiquitin may be imaged directly.

In a particularly preferred embodiment, antibodies that bind the insulin receptor are immobilized on a solid substrate, e.g., wells of a microtiter plate and contacted with cell extracts for a time and under conditions sufficient for an antigen-antibody complex to form thereby capturing the insulin receptor. After washing away unbound proteins, the wells are either directly imaged (e.g., for reactions performed with fluorescent or

radio-labeled ubiquitin) or contacted with anti-ubiquitin antibody for a time and under conditions sufficient for an antigen-antibody complex to form. Binding of the anti-ubiquitin antibody is detected using a second antibody conjugated to horse-radish peroxidase enzyme or other detectable label.

5

The assay may be conducted in replica plates e.g., in the presence or absence of a series of compounds being tested to facilitate comparison of the amount of ubiquitination of the receptor in the presence and absence of the compound being tested.

10 In a further embodiment, a first replica plate is contacted with second antibody after capturing the insulin receptor and a second replica plate is contacted with a second antibody after binding of the anti-ubiquitin antibody. In accordance with this embodiment, measurement of the ratio of the amount of second antibody bound to the first and second replica plates indicates the amount of ubiquitinated insulin receptor
15 relative to the total amount of insulin receptor in the cell or sample. Such measurement is particularly useful for correcting for sample variations. To facilitate high throughput analyses, it is particularly preferred for the second antibodies to be labelled with different colored dyes or fluorophores to permit their simultaneous detection.

20

A further aspect of the present invention provides methods for determining a modulator of the activity, formation or stability of a protein complex selected from the group consisting of: (i) a Cbl-APS complex; (ii) a Cbl-CAP complex; (iii) a Cbl-CAP-flotillin complex; (iv) a Cbl- C3G complex; (v) a Cbl-CrkII complex; and (vi) a Cbl-C3G-
25 CrkII complex.

In their general form, the methods of the present invention comprise determining the association or dissociation of the protein complex, or the structure of the complex, in the presence and absence of a candidate compound or a candidate
30 antibody. In accordance with the embodiment described herein, a modified association, dissociation, or structure, of the protein complex in the presence of a candidate compound or a candidate antibody indicates that the candidate is a modulator of the protein complex.

The association, dissociation, or structure of the complex may be determined by direct means, such as, for example, by determining real time association or dissociation constants in the presence and absence of the candidate, or modified binding of an antibody that recognizes a conformational epitope of the complex.

- 5 Biosensors used essentially as described herein above, in the presence or absence of the candidate compound or antibody, are particularly suited to such applications.

Alternatively, the association, dissociation, or structure of the complex may be determined by indirect means, such as, for example, using a protein recruitment
10 system, n-hybrid screen, reverse n-hybrid screen, plate agar diffusion assay, ELISA, or other well known assay format for detecting protein-protein interactions. Such indirect means generally use a reporter system to detect formation or dissociation of the protein complex.

- 15 Standard solid-phase ELISA assay formats are particularly useful for identifying antagonists of the protein-protein interaction. In accordance with this embodiment, one of the binding partners (e.g. APS or CAP or CrklI or C3G or a portion thereof) is immobilized on a solid matrix, such as, for example an array of polymeric pins or a glass support. Conveniently, the immobilized binding partner is a fusion polypeptide
20 comprising Glutathione-S-transferase (GST; e.g. a CAP-GST fusion), wherein the GST moiety facilitates immobilization of the protein to the solid phase support. The second binding partner (e.g. Cbl) in solution is brought into physical relation with the immobilized protein to form a protein complex, which complex is detected using antibodies directed against the second binding partner. The antibodies are generally
25 labeled with fluorescent molecules or conjugated to an enzyme (e.g. horseradish peroxidase), or alternatively, a second labeled antibody can be used that binds to the first antibody. Conveniently, the second binding partner is expressed as a fusion polypeptide with a FLAG or oligo-histidine peptide tag, or other suitable immunogenic peptide, wherein antibodies against the peptide tag are used to detect the binding
30 partner. Alternatively, oligo-HIS tagged protein complexes can be detected by their binding to nickel-NTA resin (Qiagen), or FLAG-labeled protein complexes detected by their binding to FLAG M2 Affinity Gel (Kodak). It will be apparent to the skilled person that the assay format described herein is amenable to high throughput screening of

samples, such as, for example, using a microarray of bound peptides or fusion proteins.

A two-hybrid assay is described in US Patent No. 6,316,223 to Payan *et al.*,
5 incorporated herein by reference. The basic mechanism described by Payan *et al.* is
similar to the yeast two hybrid system. In the two-hybrid system, the binding partners
are expressed as two distinct fusion proteins in a mammalian host cell. In adapting
the standard two-hybrid screen to the present purpose, a first fusion protein consists of
10 a DNA binding domain which is fused to one of the binding partners, and a second
fusion protein consists of a transcriptional activation domain fused to the other binding
partner. The DNA binding domain binds to an operator sequence which controls
expression of one or more reporter genes. The transcriptional activation domain is
recruited to the promoter through the functional interaction between binding partners.
Subsequently, the transcriptional activation domain interacts with the basal
15 transcription machinery of the cell, thereby activating expression of the reporter
gene(s), the expression of which can be determined. Candidate bioactive agents that
modulate the protein-protein interaction between the binding partners are identified by
their ability to modulate transcription of the reporter gene(s) when incubated with the
host cell. Antagonists will prevent or reduce reporter gene expression, while agonists
20 will enhance reporter gene expression. In the case of small molecule modulators,
these are added directly to the cell medium and reporter gene expression determined.
On the other hand, peptide modulators are expressible from nucleic acid that is
transfected into the host cell and reporter gene expression determined. In fact, whole
peptide libraries can be screened in transfected cells.

25

Alternatively, reverse two hybrid screens, such as, for example, described by
Vidal *et al.*, *Proc. Natl Acad. Sci USA* 93, 10315-10320, 1996, may be employed to
identify antagonist molecules. Reverse hybrid screens differ from forward screens
supra in so far as they employ a counter-selectable reporter gene, such as for
30 example, *CYH2* or *LYS2*, to select against the protein-protein interaction. Cell survival
or growth is reduced or prevented in the presence of a non-toxic substrate of the
counter-selectable reporter gene product, which is converted by said gene product to a
toxic compound. Accordingly, cells in which the protein-protein interaction of the
invention does not occur, such as in the presence of an antagonist of said interaction,

survive in the presence of the substrate, because it will not be converted to the toxic product. For example, a portion/fragment of Cbl that binds to APS or CAP or CrkII or C3G is expressed as a DNA binding domain fusion, such as with the DNA binding domain of GAL4; and the portion of APS or CAP or CrkII or C3G that binds Cbl is expressed as an appropriate transcription activation domain fusion polypeptide (e.g. with the GAL4 transcription activation domain). The fusion polypeptides are expressed in yeast in operable connection with the *URA3* counter-selectable reporter gene, wherein expression of *URA3* requires a physical relation between the GAL4 DNA binding domain and transcriptional activation domain. This physical relation is achieved, for example, by placing reporter gene expression under the control of a promoter comprising nucleotide sequences to which GAL4 binds. Cells in which the reporter gene is expressed do not grow in the presence of uracil and 5-fluororotic acid (5-FOA), because the 5-FOA is converted to a toxic compound. Candidate peptide inhibitor(s) are expressed in libraries of such cells, wherein cells that grow in the presence of uracil and 5-FOA are retained for further analysis, such as, for example, analysis of the nucleic acid encoding the candidate peptide inhibitor(s). Small molecule antagonists are determined by incubating the cells in the presence of the small molecules and selecting cells that grow or survive of cells in the presence of uracil and 5-FOA.

20

Alternatively, a protein recruitment system, such as that described in U.S. Patent No. 5, 776, 689 to Karin *et al.*, is used. In a standard protein recruitment system, a protein-protein interaction is detected in a cell by the recruitment of an effector protein, which is not a transcription factor, to a specific cell compartment. Upon translocation of the effector protein to the cell compartment, the effector protein activates a reporter molecule present in that compartment, wherein activation of the reporter molecule is detectable, for example, by cell viability, indicating the presence of a protein-protein interaction.

30

More specifically, the components of a protein recruitment system include a first expressible nucleic acid encoding a first fusion protein comprising the effector protein and one of the binding partners (e.g. APS or CAP or CrkII or C3G or a portion thereof), and a second expressible nucleic acid molecule encoding a second fusion protein comprising a cell compartment localization domain and the other binding partner (e.g.

Cbl or a portion thereof). A cell line or cell strain in which the activity of an endogenous effector protein is defective or absent (e.g. a yeast cell or other non-mammalian cell), is also required, so that, in the absence of the protein-protein interaction, the reporter molecule is not expressed.

5

A complex is formed between the fusion polypeptides as a consequence of the interaction between the binding partners, thereby directing translocation of the complex to the appropriate cell compartment mediated by the cell compartment localization domain (e.g. plasma membrane localization domain, nuclear localization domain, mitochondrial membrane localization domain, and the like), where the effector protein then activates the reporter molecule. Such a protein recruitment system can be practiced in essentially any type of cell, including, for example, mammalian, avian, insect and bacterial cells, and using various effector protein/reporter molecule systems.

15

For example, a yeast cell based assay is performed, in which the interaction between Cbl and one or more of its binding partners results in the recruitment of a guanine nucleotide exchange factor (GEF or C3G) to the plasma membrane, wherein GEF or C3G activates a reporter molecule, such as Ras, thereby resulting in the survival of cells that otherwise would not survive under the particular cell culture conditions. Suitable cells for this purpose include, for example, *Saccharomyces cerevisiae* cdc25-2 cells, which grow at 36°C only when a functional GEF is expressed therein, Petitjean *et al.*, *Genetics* 124, 797-806, 1990) Translocation of the GEF to the plasma membrane is facilitated by a plasma membrane localization domain. Activation of Ras is detected, for example, by measuring cyclic AMP levels in the cells using commercially available assay kits and/or reagents. To detect antagonists of the protein-protein interaction of the present invention, duplicate incubations are carried out in the presence and absence of a test compound, or in the presence or absence of expression of a candidate antagonist peptide in the cell. Reduced survival or growth of cells in the presence of a candidate compound or candidate peptide indicates that the peptide or compound is an antagonist of the interaction between Cbl and one or more of its binding partners.

25
30

A "reverse" protein recruitment system is also contemplated, wherein modified survival or modified growth of the cells is contingent on the disruption of the protein-protein interaction by the candidate compound or candidate peptide. For example, NIH 3T3 cells that constitutively express activated Ras in the presence of GEF can be used, wherein the absence of cell transformation is indicative of disruption of the protein complex by a candidate compound or peptide. In contrast, NIH 3T3 cells that constitutively express activated Ras in the presence of GEF have a transformed phenotype (Aronheim *et al.*, *Cell*. 78, 949-961, 1994)

10 In yet another embodiment, small molecules are tested for their ability to dissociate the protein complex of the invention, by an adaptation of plate agar diffusion assay described by Vidal and Endoh, *TIBS* 17, 374-381, 1999, which is incorporated herein by reference.

15 A further embodiment of the invention provides a method for determining a modulator of an interaction between Cbl or a portion of Cbl and a polypeptide selected from the group consisting of APS, CAP, CrkII and C3G or a portion of said polypeptide, said method comprising:

- 20 (i) determining the level of a protein complex selected from the group consisting of: (i) a complex comprising Cbl and APS; (ii) a complex comprising Cbl and CAP; (iii) a complex comprising Cbl and CrkII; (iv) a complex comprising Cbl and C3G; (v) a complex comprising Cbl and CAP and flotillin; and (vi) a complex comprising Cbl and CrkII and C3G in the absence of a candidate compound or candidate antibody; and
- 25 (ii) determining the level of said protein complex in the presence of a candidate compound or in the presence of said candidate antibody
- wherein a difference in the level of said protein complex at (i) and (ii) indicates that the candidate compound or candidate antibody is a modulator of said interaction.

30 This embodiment of the invention applies *mutatis mutandis* to the determination of protein complexes comprising a portion of any one or more of the protein binding partners (i.e. Cbl, APS, CAP, CrkII or C3G).

It will be understood by those skilled in the art that any one or more of the assay methods for antagonists as described herein above can be adapted for this purpose. This is because the level of the protein complex in the presence or absence of a candidate compound or antibody is related to antibody binding in the case of
5 ELISAs, or to cell survival or growth, in the case of hybrid screens or protein recruitment assays. ELISA-based assay formats are particularly suitable for this purpose, because they are readily quantifiable, by calibrating the detection system against known amounts of a protein standard to which the antibody binds. Such quantitation is well known to the skilled person.

10

It is to be understood that the modulators can be antagonists or inhibitors of complex formation or stability, or alternatively, agonists or promoters of complex formation and stability.

15

The modulators identified using the methods described herein are useful for the therapeutic or prophylactic treatment of diseases associated with associated with Cbl function, such as, for example, modifying fat deposition or lean muscle mass or the ratio of body fat to muscle or metabolic rate or aberrant glucose uptake or feeding behavior. In one embodiment, the compounds are used to treat a condition selected
20 from the group consisting of: hyperglycemia, hyperinsulinemia, obesity, adult-onset obesity, non-insulin-dependent diabetes mellitus, type II diabetes, glucose intolerance, and hypertrophy or hyperplasia of the islets of Langerhans.

In another embodiment, the compounds are used for cosmetic purposes, for
25 example, by bodybuilders or persons wishing to modify their weight or body content of fat or muscle.

Accordingly, another aspect of the invention provides a method comprising administering an effective amount of a Cbl antagonist to an animal or human subject to
30 inhibit or reduce the expression or activity of Cbl in the subject. Preferably, the subject is a subject in need of treatment, such as a subject suffering from a condition selected from the group consisting of: elevated glucose uptake, reduced appetite or dietary intake, hyperglycemia, hyperinsulinemia, enhanced fat deposition or obesity, adult-

onset obesity, non-insulin-dependent diabetes mellitus, type II diabetes, glucose intolerance, and hypertrophy or hyperplasia of the islets of Langerhans.

In one embodiment, the invention also provides a method of treating a feeding disorder characterized by reduced dietary intake or suppressed appetite in a subject said method comprising administering to the subject an amount of a Cbl antagonist effective to enhance the appetite or dietary intake of the subject. The method of the invention is particularly suited to the treatment of anorexia or bulimia.

In a related embodiment, the invention also provides a method of treating a feeding disorder characterized by reduced dietary intake or suppressed appetite in a subject said method comprising administering to the subject an amount of a compound that reduces expression of functional Cbl effective to enhance the appetite or dietary intake of the subject.

Preferably, the compound or Cbl antagonist is a compound or antagonist identified using a screening method described herein.

To determine an appropriate dosage for treatment, data from the cell culture assays or animal studies are used, wherein a suitable dose is within a range of circulating concentrations that include the ED_{50} of the active compound with little or no toxicity. The dosage may vary within this range depending upon the dosage form employed and the route of administration utilized. For any Cbl inhibitor or antagonist used in the method of the invention, the therapeutically effective dose can be estimated initially from cell culture assays. A dose may be formulated in animal models (e.g. any one or more of the mouse models described *supra* having genetic obesity-diabetes syndromes, such as hyperglycemia, hyperinsulinemia, and obesity) to achieve a circulating plasma concentration range that includes the IC_{50} (i.e., the concentration of the test Cbl inhibitor which achieves a half-maximal inhibition of symptoms) as determined in cell culture. Such information can be used to more accurately determine useful doses in humans. Levels in plasma maybe measured, for example, by high performance liquid chromatography.

In an alternative embodiment, the present invention provides for the use of a Cbl antagonist in the preparation of a medicament for the treatment of a condition selected from the group consisting of: elevated glucose uptake, reduced appetite or dietary intake, hyperglycemia, hyperinsulinemia, enhanced fat deposition or obesity, adult-onset obesity, non-insulin-dependent diabetes mellitus, type II diabetes, glucose intolerance, and hypertrophy or hyperplasia of the islets of Langerhans.

The various embodiments of the invention described herein for identifying compounds that are administered to animals are also suitably performed using isolated cells that have been previously derived from the animal or readily available as isolated cells, the only requirement being that the cell possesses the required Cbl phenotype to perform the assay. In one embodiment, the isolated cells are skeletal muscle cells, cardiac muscle cells, fibroblasts or fat cells (adipocytes). In lieu of using wild-type or normal animals having no Cbl deficiency, 3T3-L1 adipocytes can be used. The various embodiments apply *mutatis mutandis* to the use of such isolated cells.

The present invention is further described with reference to the following examples and the accompanying drawings.

Example 1

Methods

Animals were housed at the BTF facility of the Garvan Institute of Medical Research, Sydney, New South Wales, Australia. All procedures undertaken in these animals have been reviewed by the Ethics committee of the Garvan Institute. Animals were fed *ad libitum* with standard rodent chow and housed in 12 hour light/dark cycle. Body weight and food intake were monitored weekly for 12 weeks from weaning.

For determining glucose tolerance, animals were fasted overnight. Glucose (2 g/kg body weight) was administered into the intraperitoneal cavity following removal of a blood sample to test basal glucose concentration. Blood samples were taken at 15

min intervals for the following 90 min. Glucose assay was performed using the glucose oxidase method.

Fasting blood samples were also taken for measurement of circulating lipids and cytokines. Adipose depots, muscle, liver, brain were excised and weighed and frozen for subsequent biochemical analyses.

Temperature was measured using a Rectal probe (BAT-10, Physitemp) at the beginning and the end of the light cycle.

10

For determining glucose transport in muscle and adipose tissue, animals were fasted overnight and whole soleus muscle or gonadal white adipose tissue explants were incubated *in vitro* in the absence or presence of insulin in a Krebs Ringer buffer.

15

Glucose uptake was measured using the radiolabeled 2-deoxyglucose method.

20

For determining adipocyte size, the adipocytes were isolated using the collagenase method and incubated overnight in 2% osmium tetroxide at 37 C. Cells were mounted on a slide and images were acquired using bright field microscopy. Cell diameter was determine using Adobe Photoshop software.

Results

Figures 1 through 6 show that Cbl-deficient mice have significantly higher body weight and dietary intake, however reduced fat deposition and smaller adipocytes, compared to otherwise isogenic non-mutant animals of the same gender. The body temperature of Cbl-deficient animals is also enhanced. Surprisingly, and in contrast to what was expected, disruption of the Cbl gene lead to enhanced basal glucose uptake into both adipocytes and muscle cells. The results are also summarized in Table 1 below.

30

Table 1
Phenotype of Cbl-deficient mice

Parameter	Phenotype in c-Cbl ^{-/-} animals compared to wild type Cbl ^{+/+} animals
Body weight	No change or slight increase in males
Food intake	Increased
Fat mass	Reduced
Adipocyte size	Reduced
Glucose tolerance	Increased
Temperature	Increased
Glucose transport into fat	Increased I
Glucose transport into muscle	Increased I
Fasting blood glucose	No change

In two independent experiments, the average body temperature of Cbl-deficient males and females increased as indicated in Table 2 below:

Table 2
Enhanced body temperature in Cbl-deficient animals (Average °C ± SEM)

Experiment No.	Males		Females	
	Cbl ^{+/+}	Cbl ^{-/-}	Cbl ^{+/+}	Cbl ^{-/-}
1	37.11°C ± 0.26°C	38.93°C ± 0.22°C	37.60°C ± 0.30°C	38.06°C ± 0.15°C
2	37.25°C ± 0.16°C	38.17°C ± 0.14°C	37.62°C ± 0.09°C	37.31°C ± 0.12°C

EXAMPLE 2

Glucose transport in muscles isolated from c-CBL^{-/-} mice

Overnight fasted mice (16-18 weeks old) were sacrificed by cervical dislocation and the soleus muscles (SOL) and extensor digitorum longus (EDL) muscles removed immediately for incubation *in vitro*. After excision, SOL and EDL were transferred to individual 25 ml flasks containing 2 ml of oxygenated medium placed in a shaking water bath at 30°C. All incubation media were prepared from a pre-gassed (95% O₂/5% CO₂) stock of Krebs-Henseleit Bicarbonate buffer (KHB) (118.5 mM NaCl, 24.7 mM NaHCO₃, 4.74 mM KCl, 1.18 mM MgSO₃, 1.18 mM KH₂PO₄ and 2.5 mM CaCl₂, pH 7.4) supplemented with 2mM pyrovate, 8 mM mannitol and 0.1% w/v bovine serum albumin (BSA). The gas phase in the flasks was maintained at 95% O₂/5% CO₂ throughout the experiment.

The muscles were allowed to recover for 10 min. after removal of the final muscle. A 2-deoxyglucose (2-DOG) uptake assay was performed with 16 muscles from 4 mice at a time. Muscles were placed in new media without insulin, or with 300 µU/ml (2.2 nM) insulin or with 10000 µU/ml (72 nM) insulin for 30 min. An insulin concentration of 300 µU/ml was selected, as this was the insulin level found to elicit half-maximal insulin-stimulated glucose uptake in SOL in a pilot experiment. An insulin concentration of 10000 µU/ml was used to ensure maximal insulin-stimulated glucose transport.

Following the 30 min. incubation period, the medium was changed to KHB containing 2 mM pyrovate, 8 mM mannitol, 0.1% w/v BSA, 1 mM 2-DOG, [1-¹⁴C]-Mannitol and 2-[2-6 ³H]-DOG (Amersham Pharmacia Biotech Inc., Little Chalfon, U.K.) to a specific activity of 0.128 µCi/ml and 0.083 µCi/ml, respectively. When present, the insulin concentration was the same as during the previous 30 min. incubation period. Labeled 2-DOG diffuses into muscle cells through sarcolemmal glucose transporters and is trapped as 2-DOG-6-phosphate while diffusion of labeled mannitol across the plasma membrane is limited, making it suitable as an extracellular marker. After 16 min. exposure to isotopes, muscles were briefly washed in ice-cold KHB, blotted on paper, placed in Eppendorf tubes, and immediately frozen in liquid nitrogen. Muscles were stored at -80°C until processed.

Frozen muscles were weighed and transferred to fresh Eppendorf tubes. After addition of 250 μ l of 1 N NaOH the muscles were incubated at 65°C with occasional vortexing until dissolved. Then 250 μ l of 1 N HCl was added and samples were
5 centrifuged at 17000 g for 3 min. Aliquots of 350 μ l of the resultant supernatant supernatant, or an aliquot of a standard (5 μ l of [1-¹⁴C]-Mannitol and 2-[2-6 ³H]-DOG in 10 ml Milli Q water), or an aliquot of media or background samples (Milli Q water) were transferred to β -scintillation vials. Then 4.5 ml of scintillation liquid (Ultima Gold XR, Perkin Elmer Life Sciences, Boston, MA, USA) was added to each vial and, after
10 mixing, the tubes were counted for 3 min. each in a β -scintillation counter (Beckman LS6000 SC, Beckman Coulter, Inc. Fullerton, CA, U.S.A.).

As shown in Figure 7 the rate of 2-deoxyglucose uptake was significantly upregulated in SOL isolated from c-CBL^{-/-} mice compared to c-CBL^{+/+} controls,
15 indicating an enhanced metabolic rate in c-CBL deficient mice. In the presence of 300 μ M/ml insulin (submax), the amount of 2-deoxyglucose uptake was significantly increased in both SOL and EDL isolated from c-CBL^{-/-} mice compared to c-CBL^{+/+} mice. When exposed to sufficient levels of insulin to ensure maximal insulin-stimulated glucose transport (ie. 1000 μ U/ml insulin) there was a significant increase in
20 2-deoxyglucose transport in SOL isolated from c-CBL^{-/-} mice compared to c-CBL^{+/+} mice.

These results indicate that c-CBL^{-/-} mice have increased insulin-stimulated glucose uptake (approximately 30% increase) in isolated SOL and EDL muscles,
25 thereby indicating that c-CBL^{-/-} mice have increased peripheral insulin sensitivity.

EXAMPLE 3

Glucose transport in fat explants from c-CBL^{-/-} mice

Animals were sacrificed as described in Example 2 and epididymal fat pads
5 were excised and placed in 15 ml tubes containing Hepes Krebs Ringer Phosphate
Buffer (HKRP) (12.5 mM HEPES/pH 7.4, 120 mM NaCl, 6 mM KCl, 1.2 mM Mg SO₄, 1
mM CaCl₂, 0.4 mM NaH₂PO₄, 0.6 mM Na₂ HPO₄) supplemented with 2 mM sodium
pyruvate and 2% BSA. The tissue was then minced using scissors until pin-head size
pieces were obtained. Approximately 50 µl of fat explants were placed in 24-well plate
10 wells containing 0.45 ml of HKRP buffer. Explants were incubated in the absence or
presence of 0.05 nM or 1 nM insulin for 15 minutes at 37°C. Glucose transport was
assayed using the 2-deoxyglucose method essentially as described in Example 2. The
assay was initiated by the addition of 100 µM 2-Deoxy-[³H] glucose (1.5 µCi/ml). Non-
specific 2-Deoxy-[³H] glucose uptake was determined in the presence of Cytochalasin
15 B (50 µM). After 10 min, the assay was terminated by washing the cells rapidly three
times with ice-cold phosphate-buffered saline (PBS). Fat explants in wells were
collected and weighed. Explants were then placed in vials containing scintillation liquid
and counted next morning as described above. ³H cpm were normalised by tissue
weight. Statistical analysis was performed using the Student's t test (Sigma Plot
20 software).

As shown in Figure 8 the amount of 2-deoxyglucose incorporated into fat
explants from c-CBL^{-/-} (KO) mice was increased in the presence of both 0.05nM and
0.1nM of insulin compared to c-CBL^{+/+} (WT) mice. These data indicate that c-CBL^{-/-}
25 mice have increased insulin-stimulated glucose uptake in fat explants compared to c-
CBL^{+/+} mice, indicating increased peripheral insulin sensitivity in knockout mice.

EXAMPLE 4

Measurement of resting metabolic rate of c-CBL^{-/-} mice

Measurement of resting metabolic rate (i.e., muscle thermogenesis) of mice was performed essentially as described in Withers, P. C. *Australian Journal of Zoology* 49:445-461, 2001. Briefly, open-circuit respirometry was used to measure the rates of oxygen consumption (VO₂) and carbon dioxide production (VCO₂) at a controlled temperature of 25 (+/- 1°C).

Mice were removed from their nest box, weighed to ± 0.1 g and then placed into a metabolic chamber that consisted of a 500 ml glass jar sealed with a rubber stopper. Compressed air was passed through the chamber at 400 mL min⁻¹, controlled by a Brooks 5871-A mass-flow controller, to maintain levels of O₂ above 20% and CO₂ below 1%. Excurrent air passed through a column of drierite to remove water vapour, then through a Qubit S152 infrared CO₂ analyser then a Servomex OA 184 paramagnetic O₂ analyser. At the conclusion of the trial, the mouse was removed from the chamber and its Tb was measured immediately using a plastic-sheathed thermocouple with a RS Components 611234 thermocouple meter. Baseline values of background O₂ and CO₂ were established for at least 15 min before and after each metabolic trial. Analog voltage outputs were recorded using Protek 506 (for CO₂) and Thurlby 1905a (for O₂) digital multimeters, and their RS232 outputs were recorded with a PC using a custom Visual Basic program. The metabolic system was calibrated using a butane flame (Withers 2001). Resting VO₂ and VCO₂ were determined using a custom Visual Basic program, using the formulae of Withers (2001).

As shown in Table 3 c-CBL^{-/-} mice show increased oxygen consumption compared to c-CBL^{+/+} mice, ie. c-CBL^{-/-} mice show increased VO₂ and VCO₂.

The increased oxygen consumption observed in c-Cbl^{-/-} animals indicate an elevation of resting metabolic rate. This result is consistent with lower plasma and tissue lipid levels observed in c-Cbl^{-/-} mice compared to c-Cbl^{+/+} animals (as described in Examples 2 and 3).

Table 3
Analysis of metabolic rate of cCBL^{-/-} mice

	Tb (°C)	VO2 (ml/g/h)	VCO2 (ml/g/h)	RQ	conductance	
WT						
	36.7	3.5	2.96	0.85	0.272	mean
	0.318	0.120	0.121	0.05	0.009	se
	P<0.02	P<0.001	P<0.002	P<0.04	P<0.01	
c-CBL KO	37.6	4.6	3.7	0.8	0.36	mean
	0.2	0.22	0.2	0.022	0.02	se

EXAMPLE 5

Development of an *in vitro* assay for determining Cbl E3 ubiquitin ligase activity

Antibodies

- 5 Anti-ubiquitin antibody is obtained from Santa Cruz Laboratory. Anti-insulin receptor antibody 83-14 is obtained from Abcam, Inc, Cambridge MA 02139, USA.

*Expression vectors and cell lines*CHO.T-APS cells

- 10 CHO.T cells (Ebina *et al.*, *Proc. Natl Acad. Sci USA* 82, 8014-8018, 1985) stably-expressing a Myc-tagged rat APS from the vector pIRES Hygro (Clontech) are produced as described by Ahmed *et al.*, *FEBS Letts* 475, 31-34, 2000. Briefly, the Myc-tagged APS (Qian *et al.*, *Neuron* 21, 1017-1029, 1998) is subcloned into pIRES Hygro and transfected into CHO.T cells using Superfect (Qiagen), and transfected
15 cells are selected in media comprising about 800 µg/ml hygromycin. Clones are purified by limiting dilution and screened using anti-myc 9E10 monoclonal antibody prepared from a publicly available 9E10 hybridoma. Clones are maintained in media comprising about 400 µg/ml hygromycin.

CHO.T-APS cells expressing human c-Cbl and dominant negative c-Cbl mutants

- 20 Several dominant-negative mutants of human c-Cbl are described in the literature, including c-Cbl G306E (SEQ ID NO: 248), c-Cbl C381A (SEQ ID NO: 250), c-Cbl Y700F (SEQ ID NO: 252), c-Cbl Y731F (SEQ ID NO: 254), c-Cbl Y774F (SEQ ID NO: 256) and c-Cbl 480 (SEQ ID NO: 260). These known mutants provide useful negative controls to assess the ability of a putative inhibitor of c-Cbl-mediated
25 ubiquitination of IR-β in isolated cells. Accordingly, the open reading frames encoding these dominant negative mutants (SEQ ID Nos: 247, 249, 251, 253, 255 and 259, respectively) are separately sub-cloned into the retroviral expression vector pBabe-Puro retroviral expression vector (Morgenstern and Land, *Nucleic Acids Res.* 18, 3587-3596, 1990), to produce the control vectors pBabe-Cbl G306E, pBabe-C381A
30 pBabe-Cbl Y700F, pBabe-Cbl Y731F, pBabe-Y774F and pBabe-Cbl 480.

A further control plasmid comprising the full-length human c-Cbl open reading frame is also produced in the pBabe vector.

A test plasmid is also produced that are capable of expressing a further putative dominant negative mutant of human c-Cbl, designated c-Cbl Y700F/Y731F/Y774F (SEQ ID NO: 258). This mutant has mutations in the open reading frame of c-Cbl that result in three tyrosine residues that would normally be phosphorylated being substituted for phenylalanine. The nucleotide sequence of the open reading frame encoding c-Cbl Y700F/Y731F/Y774F is set forth in SEQ ID NO: 257. The mutant is produced using the Stratagene Quick Change mutagenesis kit according to the manufacturer's instructions. Confirmation of the correct mutations is obtained by standard sequence analysis. The open reading frame encoding c-Cbl Y700F/Y731F/Y774F is cloned into pBabe-Puro, to produce the test vector pBabe- Cbl Y700F/Y731F/Y774F.

BOSC23 packaging cells (Pear *et al.*, *Proc. Natl. Acad. Sci. USA*, 90, 8392-8396, 1993) are maintained in DMEM containing 10% FBS at 37 °C in a humidified atmosphere of 10% CO₂. Cells are then transfected by calcium phosphate co-precipitation with 10 µg each of the plasmids.

Transiently produced viral supernatants are used to infect CHO.T-APS cells in the presence of 4 µg/ml Polybrene. After elimination of uninfected cells by puromycin, stable cell lines are maintained in DMEM containing 10% FBS.

Alternatively, CHO.T-APS cells are transfected using Superfect (Qiagen), and transfected cells are selected, purified by limiting dilution and maintained in media comprising puromycin and 400 µg/ml hygromycin.

25 CHO.T-APS cells expressing siRNAs and shRNAs targeting human c-Cbl expression

The native human c-Cbl gene sequence (SEQ ID NO: 261; GenBank Accession No. X57110) was analyzed using the siRNA Target Finder software available from Ambion, Inc. (Austin, Texas, USA) to determine those sequences most likely to silence c-Cbl expression when used to produce siRNA and/or shRNA (Table 4; SEQ ID NOs: 2-239). Further sequence analysis using the BLAST programme indicated that several

of these sequences were not present in the murine c-Cbl gene, in particular SEQ ID NOS: SEQ ID Nos: 57-59, 117-121, 175-177 and 235-239.

Oligonucleotides molecules are chemically synthesised that consist of the
5 nucleotide sequences set forth in Table 4. The sense and antisense strands of the siRNA molecules set forth in are annealed and introduced directly into CHO.T-APS cells. Briefly, CHO.T-APS cells are seeded onto 96 well tissue culture plates approximately 24 hr before transfection and grown to approximately 30–70% confluence. Prior to transfection, single stranded siRNA molecules are diluted in
10 OPTI-MEM I reduced serum medium (Ambion) to a final concentration of approximately 0.5µM. siRNA solutions are then added to siPORT Lipid (Ambion) that has been previously diluted in OPTI-MEM I reduced serum medium. This final solution is then incubated at room temperature for approximately 20 minutes.

15 The CHO.T-APS cells are then washed with OPTI-MEM I reduced serum medium and overlaid with fresh OPTI-MEM I reduced serum medium. The transfection agent/siRNA complex is then added to each well of the plate, and plates incubated for 4 hours at 37°C supplemented with 5% CO₂. Following 4 hours additional DMEM (supplemented with 10% FBS) is added to each well, and cells
20 cultured at 37°C supplemented with 5% CO₂.

For construction of shRNA, a loop sequence (TTCAAGAGA, SEQ ID NO: 246) is positioned between complementary sense and antisense strands (SEQ ID NOS: 4-239) to facilitate hairpin formation. Oligonucleotides that are complementary to the
25 assembled shRNA are also produced synthetically. Both strands of each shRNA molecule are then mixed in equimolar amounts, heated to 95°C for 10 minutes and allowed to cool. Double stranded shRNA-encoding DNAs are cloned into the pAdTrack-HP expression vector (Zhap *et al.*, *Gene* 316: 137-141, 2003), upstream of the Pol III transcriptional termination sequence. The pAdTrack-HP expression vector
30 comprises *Bgl*II and *Hind*III recognition sequences to facilitate directional cloning of shRNA upstream of the Pol III transcriptional terminator.

Control plasmids comprising the full-length human c-Cbl open reading frame in the sense and antisense orientations are also produced in the pAdTrack-HP expression vector.

- 5 Adenoviruses comprising the shRNA constructs are produced essentially as described by He *et al.*, *Proc. Natl. Acad. Sci. USA*. 95: 2509-2514, 1998. Briefly, the control vectors and the library of pAdTrack-shRNA vectors are linearized with *PmeI* and transfected into AdEasier-1 cells or *E. coli* BJ5183 cells carrying the pAdEasy-1 plasmid. The pAdEasy-1 adenoviral plasmid contains all Ad5 sequences except
- 10 nucleotides 1-3,533 (encompassing the E1 genes) and nucleotides 28,130-30,820 (encompassing E3). Recombinant viral genomes are linearized with *PacI* and transfected into 293 cells in a six-well plate using lipofectamine 2000 (Invitrogen). Eight days after transfection, the recombinant virus is collected and subjected to one round of amplification in a T-25 flask with 1.5×10^6 293 cells, resulting in 2 ml of viral
- 15 stocks. CHO.T-APS cells in a 96-well plate are infected with Adenovirus comprising the pAdTrack-shRNA library for 2h, washed, and incubated with medium for 4 days.

Lysate preparation and Sandwich ELISA assay

- CHO.T-APS cells produced as described *supra* to express APS in the
- 20 presence or absence of a dominant negative c-Cbl protein or siRNA or shRNA against human c-Cbl are stimulated with insulin at 37°C for 10-60 mins, and lysates prepared as described by Kotani *et al.*, *Biochem J.* 335, 103-109, 1998; and Ahmed *et al.*, *Biochem J.*, 341, 665-668, 1991. Briefly, cells are washed in ice-cold phosphate-buffered saline and then lysed for about 30 min at 4°C with buffer containing 50mM
- 25 Tris-HCl, pH 8.0, 135 mM NaCl, 1% Triton X-100, 1.0 mM EDTA, 1.0 mM sodium pyrophosphate, 1.0 mM sodium orthovanadate, 10mM NaF and protease inhibitors (Roche Diagnostics; 1 tablet per 7 ml buffer).

- Anti-insulin receptor antibody 83-14 is diluted in coating solution (50 mM sodium carbonate, pH 9.6; or 20 mM Tris-HCl, pH 8.5; or 10 mM PBS, pH 7.2) to a
- 30 concentration of about 1-10 µg/ml protein. The diluted antibody is adsorbed onto the wells of 96 or 256 well microtiter plates by adding 50-100 µl antibody in coating solution to the wells and incubating for about 1 hour at room temperature. The plates

are emptied and then 300 µl blocking solution (1-10% (w/v) BSA in coating solution, or 1-10% (w/v) nonfat dry milk in coating solution, or 1-10% (w/v) casein in coating solution, or 1-10% (w/v) gelatin in coating solution) is added to the wells. The plates are incubated again at room temperature for about 1 hour. The plates are emptied
5 and then washed 3-5 times using 300 µl wash solution (0.1 M phosphate-buffered saline or Tris-buffered saline (pH 7.4), 0.02%-0.05% (v/v) Tween 20) per wash. Cell lysates are added to the wells of replica plates, optionally comprising 1-10% (w/v) BSA, and the plates are incubated at 4°C overnight or at room temperature for 1 hour to overnight. The plates are again emptied and washed as 3-5 times as before. Anti-
10 ubiquitin antibody at a concentration 0.1-1.0 µg/ml protein in 1X blocking solution is added to the wells and the plates are incubated for about 1 hour at room temperature. Plates are again washed as before.

To detect the anti-ubiquitin antibody bound to the plates, a tertiary antibody solution comprising goat anti-mouse Ig conjugated to horseradish peroxidase enzyme
15 (e.g., Alpha Diagnostic International, Inc., San Antonio, TX 78238 USA) is employed. The tertiary antibody is diluted in 1X blocking solution at a final concentration of about 0.1-1.0 µg/ml protein. About 100 µl diluted tertiary antibody is added to each well, and plates are incubated for about 1 hour at room temperature. Plates are again emptied and washed, and reacted with horseradish peroxidase enzyme substrate (KPL,
20 Gaithersburg, MA 20879-4174, USA). Reactions are stopped and the absorbances of each well is determined using a plate reader. Wavelengths used will depend on the substrate employed e.g., ABTS (405-410 nm), TMB (non-stopped 620-650 nm, stopped 450 nm), OPD (non-stopped 450 nm, stopped 490 nm), pNPP (405-410 nm), BluePhos[®] (595-650 nm).

25

Results

Cell lysates derived from non-transfected CHO.T-APS cells or CHO.T-APS cells transfected with control vectors expressing human c-Cbl in the sense orientation will have detectable levels of insulin-induced ubiquitination of the insulin receptor, as
30 determined by sandwich ELISA. In marked contrast, cell lysates derived from cells comprising the dominant-negative mutant constructs pBabe-Cbl G306E, pBabe-C381A pBabe-Cbl Y700F, pBabe-Cbl Y731F, pBabe-Y774F and pBabe-Cbl 480 will

bind reduced or non-detectable levels of anti-ubiquitin antibody following antibody-capture of the insulin receptor. Cell lysates from cells transfected with the pBabe-C381A vector, which carries a mutation in the RING domain of c-Cbl, will have particularly low levels of ubiquitinated insulin receptor.

5 Such data suggest that insulin-induced CHO.T-APS cells provide a useful cellular system for assaying c-Cbl-mediated ubiquitination of the insulin receptor. Such data also suggest that the sandwich ELISA provides a useful screen for identifying agonists and antagonists of c-Cbl-mediated ubiquitination of the insulin receptor.

10 Proceeding on this basis, cells expressing a c-Cbl antisense RNA or the dominant negative mutant c-Cbl Y700F/Y731F/Y774F are introduced into CHO.T-APS cells and insulin-induced ubiquitination of the insulin receptor is assayed as for the control plasmids using the sandwich ELISA assays herein. Reduced levels of ubiquitin bound to the insulin receptor relative to the level of ubiquitin bound to the
15 receptor in lysates from cells expressing the full-length c-Cbl open reading frame in the sense orientation, indicate that these molecules are also effective antagonists of c-Cbl-mediated ubiquitination.

 Additionally, an Adenovirus (Ad5) library that express a series of pADTrack-shRNAs designed against human c-Cbl expression (Table 4) is shotgun-cloned into
20 CHO.T-APS cells, and insulin-induced ubiquitination of the insulin receptor is determined. A control plasmid comprising the full-length open reading frame of wild-type human c-Cbl is also introduced. Empty vector controls and non-transfected controls are also employed. Those cells that produce lysates having reduced levels of ubiquitinated insulin receptor as determined by sandwich ELISA are retained for
25 further analysis, such as for introduction into animal models for validation. Alternatively, or in addition, the corresponding shRNAs are introduced into C2C12 cells in the pBabe vector for assessment of their effects on muscle thermogenesis.

TABLE 4

Human c-Cbl siRNA oligonucleotides for silencing human c-Cbl gene expression

Sense strand siRNA	SEQ ID NO:	Antisense strand siRNA	SEQ ID NO:
CGTGAAGAAGAGCTCTGGGTT	4	CCCAGAGCTCTTCTTCACGTT	122
GAAGATGGTGGAGAAGTGCTT	5	GCACTTCTCCACCATCTTCTT	123
GATGGTGGAGAAGTGCTGGTT	6	CCAGCACTTCTCCACCATCTT	124
GTGCTGGAAGCTCATGGACTT	7	GTCCATGAGCTTCCAGCACTT	125
GCTCATGGACAAGGTGGTGTT	8	CACCACCTTGTCCATGAGCTT	126
GGTGGTGC GTTGTGTCA GTT	9	CTGACACAACCGCACCACCTT	127
CCCAAAGCTGGCGCTAAAGTT	10	CTTTAGCGCCAGCTTTGGGTT	128
CCCAAAGCTGGCGCTAAAGTT	11	CTTTAGCGCCAGCTTTGGGTT	129
AGCTGGCGCTAAAGAATAGTT	12	CTATTCTTTAGCGCCAGCTTT	130
AGAATAGCCACCTTATATTT	13	ATATAAGGTGGGCTATTCTTT	131
TAGCCACCTTATATCTTATT	14	TAAGATATAAGGTGGGCTATT	132
GATATGAGGGGAAGATGGATT	15	TCCATCTTCCCCTCATATCTT	133
GATGGAGACACTTGGAGAATT	16	TTCTCCAAGTGTCTCCATCTT	134
CTAAGCAAACCATAAGCCTTT	17	AGGCTTATGGTTTGCTTAGTT	135
GCAAACCATAAGCCTCTTCTT	18	GAAGAGGCTTATGGTTTGCTT	136
ACCATAAGCCTCTTCAAGGTT	19	CCTTGAAGAGGCTTATGGTTT	137
GCCTCTTCAAGGAGGGAAATT	20	TTTCCCTCCTTGAAGAGGCTT	138
GAAAGAATGTATGAGGAGATT	21	TCTCCTCATACATTCTTCTT	139
AGAATGTATGAGGAGAATTTT	22	AATTCTCCTCATACATTCTTT	140
TGTATGAGGAGAATTCTCATT	23	TGAGAATTCTCCTCATACATT	141
TTCTCAGCCTAGGCGAAACTT	24	GTTTCGCCTAGGCTGAGAATT	142
ACCTAACCAACTGTCCCTTT	25	AGGGACAGTTTGTTAGGTTT	143
CCAACTGTCCCTCATCTTTT	26	AAGATGAGGGACAGTTTGTT	144
ACTGTCCCTCATCTTCAGCTT	27	GCTGAAGATGAGGGACAGTTT	145
GGAATCTTTCCAAGTGGACTT	28	GTCCACTTGGAAAGATTCTT	146
TCTTTCCAAGTGGACTCTTTT	29	AAGAGTCCAATTGGAAAGATT	147
GTGGACTCTTTCAGGGAGATT	30	TCTCCCTGAAAGAGTCCACTT	148
AGCAGATGCTGCGGAATTTT	31	AAATTCCGCAGCATCTGCTTT	149
GACAATAGTCCCTTGGAAGTT	32	CTTCCAAGGGACTATTGTCTT	150
TAGTCCCTTGGAAGAGCTTTT	33	AAGCTCTTCCAAGGGACTATT	151
GAGCTTTTCGACAGGCTCTATT	34	TAGAGCCTGTCGAAAGCTCTT	152
GTGCATCCCATCAGTTCTGTT	35	CAGAACTGATGGGATGCACTT	153
ATCCACTATTGATCTGACCTT	36	GGTCAGATCAATAGTGGATTT	154
TTTGACATCTTTACCCGACTT	37	GTCGGGTAAAGATGTCAAATT	155
TTGGAACAGCCTTGCTGTATT	38	TACAGCAAGGCTGTTCCAATT	156
CAGCCTTGCTGTAACCTATTT	39	ATGAGTTACAGCAAGGCTGTT	157
CTCATCCTGGCTACATGGCTT	40	GCCATGTAGCCAGGATGAGTT	158
GTGAAAGCTCGGCTCCAGATT	41	TCTGGAGCCGAGCTTCACTT	159
AGCTCGGCTCCAGAAATTCTT	42	GAATTTCTGGAGCCGAGCTTT	160
ATTCATTACAAACCTGGCTT	43	GCCAGGTTTGTGAATGAATTT	1161
ACCTGGCAGTTATATCTTCTT	44	GAAGATATAACTGCCAGGTTT	162
CATTCTCCAGACAATCCCTTT	45	AGGGATTGTCTGGAGAATGTT	163
TCCCTCACAAATAACCTCTTT	46	AGAGGTTTATTGTGAGGGATT	164
TAAACCTCTCTTCCAAGCATT	47	TGCTTGGAAGAGAGGTTTATT	165

ACCTCTCTTCCAAGCACTGTT	48	CAGTGCTTGGAAGAGAGGTTT	166
GCACTGATTGATGGCTTCATT	49	TGAAGCCATCAATCAGTGCTT	167
GGCTTCTATTTGTTTCTGTT	50	CAGGAAACAAATAGAAGCCTT	168
ATCAGAATCCTGATCTGACTT	51	GTCAGATCAGGATTCTGATT	169
TCCTGATCTGACTGGCTTATT	52	TAAGCCAGTCAGATCAGGATT	170
CCAACTCCCCAAGACCATATT	53	TATGGTCTTGGGGAGTTGGTT	171
CTCCCCAAGACCATATCAATT	54	TTGATATGGTCTTGGGGAGTT	172
GACCATATCAAAGTGACCCTT	55	GGGTCACTTTGATATGGTCTT	173
AGTGACCCAGGAACAATATTT	56	ATATTGTTCTTGGGTCACTTT	174
CAATATGAATTATACTGTGTT	57	CACAGTATAATTCATATTGTT	175
TATGAATTATACTGTGAGATT	58	TCTCACAGTATAATTCATATT	176
TTATACTGTGAGATGGGCTTT	59	AGCCCATCTCACAGTATAATT	177
TGATAAGGATGTAAAGATTTT	60	AATCTTTACATCCTTATCATT	178
GGATGTAAAGATTGAGCCCTT	61	GGGCTCAATCTTACATCCTT	179
AGATTGAGCCCTGTGGACATT	623	TGTCCACAGGGCTCAATCTTT	180
TCAGAAGGTCAGGGCTGTCTT	63	GACAGCCCTGACCTTCTGATT	181
GGTCAGGGCTGTCTTTCTTT	64	AGAAAGGACAGCCCTGACCTT	182
ATTAAAGGTACTGAACCCATT	65	TGGGTTTCACTACCTTTAATT	183
AGGTACTGAACCCATCGTGTT	66	CACGATGGGTTTCACTACCTTT	184
CCCATCGTGGTAGATCCGTTT	67	ACGGATCTACCACGATGGGTT	185
ATTATGATGATGATGATGATT	68	TCATCATCATCATCATAATT	186
CGAGCTGATGATACTCTCTTT	69	AGAGAGTATCATCAGCTCGTT	187
GGAATTGGCTGGTGCCAAGTT	70	CTTGGCACCAGCCAATTCCTT	188
TTGGCTGGTGCCAAGGTGGTT	71	CCACCTTGGCACCAGCCAATT	189
CGGCCGCCCTTCTCCATTCTTT	72	AGAATGGAGAAGGCGGCCGTT	190
GTGCTTCTGCTCTTGGAAGTT	73	GTTCCAAGAGCAGAAGCACTT	191
CTGCTTCTAAGGCTGCTTCTT	74	GAAGCAGCCTTAGAAGCAGTT	192
GGCTGCTTCTGGCTCCCTTTT	75	AAGGGAGCCAGAAGCAGCCTT	193
AGACAAACCATTGCCAGTATT	76	TACTGGCAATGGTTTGTCTTT	194
ACCATTGCCAGTACCTCCCTT	77	GGGAGGTACTGGCAATGGTTT	195
TCCCGACCTCAAAGACGCCTT	78	GGCGTCTTTGAGGTCGGGATT	196
AGACGCCCTTGCCCTTGATTT	79	TACAAGGCAAGGGGCGTCTTT	197
TCCCCAAAGTACCAGTATCTT	80	GATACTGGTACTTTGGGGATT	198
AGTACCAGTATCTGCCCCATT	81	TGGGGCAGATACTGGTACTTT	199
GTTCCAGTGATCCCTGGACTT	82	GTCCAGGGATCACTGGAAGTT	200
GAGAAATTAACCAACCGGCATT	83	TGCCGGTTGGTTAATTCTCTT	201
TTAACCAACCGGCACTCACTT	84	GTGAGTGCCGGTTGGTTAATT	202
CCAACCGGCACTCACTTCCTT	85	GGAAGTGAGTGCCGGTTGGTT	203
CCGGCACTCACTTCCATTTT	86	AAATGGAAGTGAGTGCCGGTT	204
ATGGAGCCCAGACCAGATGTT	87	CATCTGGTCTGGGCTCCATT	205
GCACGTTTCACTCTGGATACTT	88	GTATCCAGACTGAACGTGCTT	206
TAGCAGCCCATTAGTAGGTTT	89	ACCTACTAATGGGCTGCTATT	207
TCAAACCTTCCTCATCTGCTT	90	GCAGATGAGGAAGGTTTGATT	208
ACCTTCCTCATCTGCCAATT	91	ATTGGCAGATGAGGAAGGTTT	209
TGCCATTTATTCTCTGGCTTT	92	AGCCAGAGAATAAATGGCATT	210
CTGCCACCTGGGGAGCAATT	93	ATTGCTCCCCAGGTGGCAGTT	211
TGTGAGGGTGAAGAGGACATT	94	TGTCCTCTTACCCTCACATT	212
GAGGACACAGAGTACATGATT	95	TCATGTACTCTGTGTCCTCTT	213
GCAATGTATAATATTCAGTTT	96	ACTGAATATTATACATTGCTT	214
TGTATAATATTCAGTCCCAT	97	TGGGACTGAATATTATACATT	215
TATTCAGTCCCAGGCGCCATT	98	TGGCGCCTGGGACTGAATATT	216
CACTGGTCCCAGGAGTCATT	99	TGACTCCTCGGGACCAGTGTT	217
TGAGGATGATGGGTATGATT	100	ATCATACCCATCATCCTCATT	218

CTCTCTCAGATATCTCTAATT	101	TTAGAGATATCTGAGAGAGTT	219
TGCCAGTCTCTCCTTTGGCTT	102	GCCAAAGGAGGAGCTGGCATT	220
CAAATGTCACTGAAGGTTCTT	103	GAACCTTCAGTGACATTTGTT	221
ATGTCACCTGAAGGTTCCCAATT	104	TGGGAACCTTCAGTGACATTT	222
GGTTCCCAAGTTCCCGAGATT	105	TCTCGGGAACCTTGCGGAACCTT	223
GTTCCCGAGAGGCCTCCAATT	106	TTGGAGGCCTCTCGGGAACCTT	224
CCATTCCCGCGGAGAATCATT	107	TGATTCTCCGCGGGAATGGTT	225
TCAACTCTGAACGGAAAGCTT	108	GCTTTCGGTTCAGAGTTGATT	226
CTCTGAACGGAAAGCTGGCTT	109	GCCAGCTTTCGGTTCAGAGTT	227
CGGAAAGCTGGCAGCTGTCTT	110	GACAGCTGCCAGCTTTCGGTT	228
AGCTGGCAGCTGTCAGCAATT	111	TTGCTGACAGCTGCCAGCTTT	229
CCTCATGAGTCAGGGGTACTT	112	GTACCCCTGACTCATGAGGTT	230
AGCTTTGGTCATTGCCAGTT	113	CTGGGCAATGACCAAAGCTTT	231
CAACATCGAGATGGCCAAATT	114	TTTGCCATCTCGATGTTGTT	232
ACATCCTCCGGGAATTTGTTT	115	ACAAATTCCCGGAGGATGTTT	233
TTTGTTTCCATTTCTTCTCTT	116	GAGAAGAAATGGAAACAAATT	234
GTGGCACCTAGAAGGGCAGTT	117	CTGCCCTTCTAGGTGCCACTT	235
GGGCAGGAGTTCTTTGGTTT	118	ACCAAAGGAACTCCTGCCCTT	236
GTCTTGCCCTCTCTGTGGGTT	119	CCCACAGAGAGGGCAAGACTT	237
GATTTCAAAGTGGTGAAATTT	120	ATTTCACTACTTTGAAATCTT	238
TGGAGCAGCTAGTATGTTTTT	121	AAACATACTAGCTGCTCCATT	239

EXAMPLE 6

ELISA for determining the effect of nucleic acid inhibitors on c-Cbl expression

5 Antibodies

Mouse antibodies against residues 595-810 of human c-Cbl protein are obtained from Clontech. Such antibodies are cross-reactive with c-Cbl proteins from chicken, dog, mouse and rat. A mouse monoclonal antibody that is reactive against residues 695-705 of human c-Cbl protein is supplied by AG Scientific, Inc. A rabbit or
 10 goat antibody that binds to the C-terminal region of human c-Cbl and is useful for detecting full-length c-Cbl protein (Santa Cruz Biotechnology, Inc).

Expression vectors and cell lines

C2C12 cells

15 C2C12 cells (ATCC CRL-1772; Yaffe *et al.*, *Nature* 270, 725-727, 1977; Yaffe *et al.*, *Differentiation* 7, 159-166, 1977) are a murine myoblast cell line that differentiates rapidly to form contractile myotubes and to produce characteristic muscle proteins. Cultures are maintained as non-confluent cultures to prevent depletion of

myoblasts. Myotube formation is enhanced when cells are grown in medium supplemented with 10% (v/v) horse serum instead of fetal bovine serum.

C2C12 cells expressing human c-Cbl and dominant negative c-Cbl mutants

The dominant-negative mutants of human c-Cbl designated c-Cbl G306E (SEQ ID NO: 248), c-Cbl C381A (SEQ ID NO: 250), c-Cbl Y700F (SEQ ID NO: 252), c-Cbl Y731F (SEQ ID NO: 254), and c-Cbl Y774F (SEQ ID NO: 256) expressed from the retroviral expression vector pBabe-Puro (Morgenstern and Land, *Nucleic Acids Res.* 18, 3587-3596, 1990), to produce the control vectors pBabe-Cbl G306E, pBabe-C381A pBabe-Cbl Y700F, pBabe-Cbl Y731F, and pBabe-Y774F, essentially as described in the preceding example.

A further control plasmid comprising the full-length human c-Cbl open reading frame is also produced in the pBabe vector.

A test plasmid is also produced that is capable of expressing a further putative dominant negative mutant of human c-Cbl, designated c-Cbl Y700F/Y731F/Y774F (SEQ ID NO: 258), as described in the preceding example.

BOSC23 packaging cells (Pear *et al.*, *Proc. Natl. Acad. Sci. USA*, 90, 8392-8396, 1993) are maintained in DMEM containing 10% FBS at 37 °C in a humidified atmosphere of 10% CO₂. Cells are then transfected by calcium phosphate co-precipitation with 10 µg each of the plasmids *supra*.

Transiently produced viral supernatants are used to infect C2C12 cells in the presence of 4 µg/ml Polybrene. After elimination of uninfected cells by puromycin, stable cell lines are maintained in DMEM containing 10% FBS.

Alternatively, C2C12 cells are transfected using Superfect (Qiagen), and transfected cells are selected, purified by limiting dilution and maintained in media comprising puromycin and 400 µg/ml hygromycin.

C2C12 cells expressing siRNAs and shRNAs targeting human c-Cbl expression

SiRNAs and shRNAs and control vectors are produced as described in the preceding example.

The siRNA oligonucleotides are introduced directly into C2C12 cells by seeding the cells onto 96 well tissue culture plates approximately 24 hr before transfection, growing the cells approximately 30–70% confluence (it is preferable to ensure that
5 confluence is not reached to prevent myoblast depletion) and immediately prior to transfection, diluting single stranded siRNA molecules in OPTI-MEM I reduced serum medium (Ambion) to a final concentration of approximately 0.5 μ M, adding the siRNA solutions to siPORT *Lipid* (Ambion) that has been previously diluted in OPTI-MEM I reduced serum medium and incubating the reaction mixture at room temperature for
10 approximately 20 minutes.

The C2C12 cells are then washed with OPTI-MEM I reduced serum medium and overlaid with fresh OPTI-MEM I reduced serum medium. The transfection agent/siRNA complex is then added to each well of the plate, and plates incubated for
15 4 hours at 37°C supplemented with 5% CO₂. Following 4 hours additional DMEM (supplemented with 10% FBS) is added to each well, and cells cultured at 37°C supplemented with 5% CO₂.

For stable introduction of shRNAs into C2C12 cells, Adenovirus comprising the
20 pADTrack-shRNA library produced as described in the preceding example is used to infect C2C12 cells in a 96-well plate for 2h, after which time the cells are washed and incubated with medium for 4 days.

Lysate preparation

25 C2C12 cells produced as described *supra* are lysed for about 30 min at 4°C with buffer containing 50mM Tris-HCl, pH 8.0, 135 mM NaCl, 1% Triton X-100, 1.0 mM EDTA, 1.0 mM sodium pyrophosphate, 1.0 mM sodium orthovanadate, 10mM NaF and protease inhibitors (Roche Diagnostics; 1 tablet per 7 ml buffer).

ELISA Assay format I

30 Cell lysates are diluted in coating solution (50 mM sodium carbonate, pH 9.6; or 20 mM Tris-HCl, pH 8.5; or 10 mM PBS, pH 7.2) to a concentration of about 0.1-10 μ g/ml protein. The diluted antigen is adsorbed onto the wells of 96 or 256 well

microtiter plates by adding 50-100 μ l antigen in coating solution to the wells and incubating for about 1 hour at room temperature. The plates are emptied and then 300 μ l blocking solution (1-10% (w/v) BSA in coating solution, or 1-10% (w/v) nonfat dry milk in coating solution, or 1-10% (w/v) casein in coating solution, or 1-10% (w/v) gelatin in coating solution) is added to the wells. The plates are incubated again at room temperature for about 1 hour. The plates are emptied and then washed 3-5 times using 300 μ l wash solution (0.1 M phosphate-buffered saline or Tris-buffered saline (pH 7.4), 0.02%-0.05% (v/v) Tween 20) per wash. Anti-Cbl antibodies at a concentration 0.1-1.0 μ g/ml protein in blocking solution are added to the wells of replica plates, and the plates are incubated at 4°C overnight or at room temperature for 1 hour to overnight. Different anti-Cbl antibodies can be added to each replica plate at this stage, for enhanced accuracy and validation of results. The plates are again emptied and washed as 3-5 times as before. To detect the anti-Cbl antibodies bound to the plates, a secondary antibody solution comprising an antibody that binds to the first antibody (e.g., goat anti-mouse Ig or goat anti-rabbit Ig) conjugated to horseradish peroxidase enzyme (e.g., Alpha Diagnostic International, Inc., San Antonio, TX 78238 USA) is employed. The secondary antibody is diluted in 1X blocking solution at a final concentration of about 0.1-1.0 μ g/ml protein. About 100 μ l diluted secondary antibody is added to each well, and plates are incubated for about 1 hour at room temperature. Plates are again emptied and washed, and reacted with horseradish peroxidase enzyme substrate (KPL, Gaithersburg, MA 20879-4174, USA). Reactions are stopped and the absorbances of the wells is read using a plate reader. Wavelengths used will depend on the substrate employed e.g., ABTS (405-410 nm), TMB (non-stopped 620-650 nm, stopped 450 nm), OPD (non-stopped 450 nm, stopped 490 nm), pNPP (405-410 nm), BluePhos $\text{\textcircled{O}}$ (595-650 nm).

ELISA Assay format II (Two-site ELISA)

A mouse, rabbit or goat anti-human Cbl antibody is diluted in coating solution (50 mM sodium carbonate, pH 9.6; or 20 mM Tris-HCl, pH 8.5; or 10 mM PBS, pH 7.2) to a concentration of about 1-10 μ g/ml protein. The diluted antibody is adsorbed onto the wells of 96 or 256 well microtiter plates by adding 50-100 μ l antibody in coating solution to the wells and incubating for about 1 hour at room temperature. The plates

are emptied and then 300 µl blocking solution (1-10% (w/v) BSA in coating solution, or 1-10% (w/v) nonfat dry milk in coating solution, or 1-10% (w/v) casein in coating solution, or 1-10% (w/v) gelatin in coating solution) is added to the wells. The plates are incubated again at room temperature for about 1 hour. The plates are emptied
5 and then washed 3-5 times using 300 µl wash solution (0.1 M phosphate-buffered saline or Tris-buffered saline (pH 7.4), 0.02%-0.05% (v/v) Tween 20) per wash. Cell lysates are added to the wells of replica plates, optionally comprising 1-10% (w/v) BSA, and the plates are incubated at 4°C overnight or at room temperature for 1 hour to overnight. The plates are again emptied and washed as 3-5 times as before. A
10 second anti-Cbl antibody that is different from the first antibody used and binds to a different part of the Cbl protein, at a concentration 0.1-1.0 µg/ml protein in 1X blocking solution, is added to the wells and the plates are incubated for about 1 hour at room temperature. Plates are again washed as before.

To detect the second anti-Cbl antibody bound to the plates, a tertiary antibody
15 solution that binds to the secondary antibody (e.g., a goat anti-mouse Ig or goat anti-rabbit Ig) conjugated to horseradish peroxidase enzyme (e.g., Alpha Diagnostic International, Inc., San Antonio, TX 78238 USA) is employed. The tertiary antibody is diluted in 1X blocking solution at a final concentration of about 0.1-1.0 µg/ml protein. About 100 µl diluted tertiary antibody is added to each well, and plates are incubated
20 for about 1 hour at room temperature. Plates are again emptied and washed, and reacted with horseradish peroxidase enzyme substrate (KPL, Gaithersburg, MA 20879-4174, USA). Reactions are stopped and the absorbances of the wells is read using a plate reader. Wavelengths used will depend on the substrate employed e.g., ABTS (405-410 nm), TMB (non-stopped 620-650 nm, stopped 450 nm), OPD (non-
25 stopped 450 nm, stopped 490 nm), pNPP (405-410 nm), BluePhos[®] (595-650 nm).

Results

Cell lysates derived from non-transfected C2C12 cells transfected with control vectors expressing human c-Cbl in the sense orientation will have detectable levels of
30 human c-Cbl, as determined by ELISA assay formats I or II. In marked contrast, cell lysates derived from cells comprising the dominant-negative mutant constructs pBabe-Cbl G306E, pBabe-C381A, pBabe-Cbl Y700F, pBabe-Cbl Y731F, or pBabe-Y774F will

bind reduced or non-detectable levels of anti-Cbl antibody in assay format I, or following antibody-capture of Cbl and subsequent two-site ELISA according to assay format II.

Such data suggest that the effects of inhibitors of c-Cbl expression can be
5 assayed directly by measuring c-Cbl protein levels in cell lysates from transfected C2C12 cells, in standard ELISA assay formats. Other immunoassay formats are also contemplated to be applicable in this respect.

Proceeding on this basis, c-Cbl protein levels are assayed in C2C12 cells expressing a c-Cbl antisense RNA or the dominant negative mutant c-Cbl
10 Y700F/Y731F/Y774F using the sandwich ELISA assays herein. Reduced levels of c-Cbl protein detectable in C2C12 cells expressing these molecules, relative to the level of ubiquitin bound to the receptor in lysates from cells expressing the full-length c-Cbl open reading frame in the sense orientation, indicate that these molecules are also effective antagonists of c-Cbl expression.

15 Additionally, an Adenovirus (Ad5) library that expresses a series of pADTrack-shRNAs designed against human c-Cbl expression (Table 4) is shotgun-cloned into C2C12 cells, and the level of c-Cbl protein is determined. A control plasmid comprising the full-length open reading frame of wild-type human c-Cbl is also introduced. Empty vector controls and non-transfected controls are also employed. Those cells that
20 produce lysates having reduced levels of c-Cbl protein as determined by ELISA assay format I and/or ELISA assay format II are retained for further analysis, such as for introduction into animal models for validation. Alternatively, or in addition, the corresponding shRNAs are introduced into C2C12 cells in the pBabe vector for assessment of their effects on muscle thermogenesis.

25

EXAMPLE 7

C2C12 cell-based assay for muscle thermogenesis

Expression vectors and cell lines

C2C12 cells (ATCC CRL-1772; Yaffe *et al.*, *Nature* 270, 725-727, 1977; Yaffe
30 *et al.*, *Differentiation* 7, 159-166, 1977) are obtained, maintained, and modified to

express human c-Cbl and dominant negative c-Cbl mutants, antisense molecules, siRNAs and shRNAs as described in the preceding example.

5 *Proton leak kinetics.*

Proton leak kinetics in C2C12 cells are determined essentially as described by Brand M. [(1995) in *Mitochondria : A practical approach* (Brown G and Cooper, C Eds) pp39-62, Oxford Univ Press Oxford.]. Cells are incubated for 30 min with 0.2 $\mu\text{Ci/ml}$ [^3H]-triphenylmethylphosphonium (TPMP), 0.2 μM TPMP and 1.5 μM taetraphenylboron as carriers, as well as 2.5 μg of oligomycin.

Respiration rates and membrane potential of cells are measured as follows: The starting point for each curve (resting metabolic rate) is determined as that measured in the presence of oligomycin. Increasing concentrations of myxothiazol (0-15 0.072 μM) are added to decrease the membrane potential and respiration rate. Finally, 2.5 μM myxothiazol and 2 μM carbonylcyanide p-trifluoromethoxy-phenylhydrazone are added to ascertain non-mitochondrial respiration. Non-mitochondrial respiration is then subtracted from total respiration to obtain an estimate of mitochondrial respiration. Membrane potential is estimated as described by St 20 Pierre *et al J. Biol. Chem.* 278, 26597-26603, 2003.

These measurements provide an assessment of mitochondrial respiration and the degree of mitochondrial uncoupling as assessed by proton leak kinetics.

25 *Results*

Non-transfected C2C12 cells, and C2C12 cells that are transfected with control vectors expressing human c-Cbl in the sense orientation, will provide a normal baseline of mitochondrial function and thermogenic activity, as determined by their proton leak kinetics. In marked contrast, C2C12 cells comprising the dominant-30 negative mutant constructs pBabe-Cbl G306E, pBabe-C381A, pBabe-Cbl Y700F, pBabe-Cbl Y731F, or pBabe-Y774F exhibit proton leak kinetics consistent with

enhanced mitochondrial respiration rates compared to non-transfected controls, or cells that ectopically express Cbl protein.

Such data suggest that the effects of inhibitors of c-Cbl expression can be assayed directly by measuring proton leak kinetics of transfected C2C12 cells.

5 Proceeding on this basis, proton leak kinetics are determined for C2C12 cells expressing a c-Cbl antisense RNA or the dominant negative mutant c-Cbl Y700F/Y731F/Y774F. Enhanced mitochondrial respiration rates of C2C12 cells expressing these molecules, relative to the respiration rates of cells expressing the full-length c-Cbl open reading frame in the sense orientation, indicate that these
10 molecules are also effective antagonists of c-Cbl expression.

Additionally, an Adenovirus (Ad5) library that expresses a series of pADTrack-shRNAs designed against human c-Cbl expression (Table 4) is shotgun-cloned into C2C12 cells, and the proton leak kinetics of the transfected cells is determined. A control plasmid comprising the full-length open reading frame of wild-type human c-Cbl
15 is also introduced. Empty vector controls and non-transfected controls are also employed. Those cells that exhibit proton leak kinetics consistent with enhanced mitochondrial respiration rates are retained for further analysis, such as for introduction into animal models for validation.

20

EXAMPLE 8

Screening assays performed in animal models

Production of a human c-Cbl knock-in mouse model

A 5'-Cbl strain 129 mouse genomic fragment containing sequences upstream
25 of the mouse c-Cbl gene (about 2-3 kbp) and including exon 1 and the 5' part of intron 1 is generated by PCR from mouse chromosomal DNA or a chromosome 9 BAC comprising the c-Cbl gene and flanking sequences. A 3'-Cbl strain 129 mouse genomic fragment, containing the 3' half of the final exon and 3'-flanking sequences of the mouse c-Cbl gene (about 2-3 kbp) is also derived by PCR.

30

Human genomic fragments, containing the 3' part of intron 1 through to and including the final exon of the human c-Cbl gene are isolated by sequential digestion from plasmids.

5 To obtain gene targeting constructs, the 5'-Cbl mouse genomic fragment and the human genomic fragments are inserted into a pPN2T vector (Paszty *et al.*, *Nat. Genet.* 11, 33-39, 1995) upstream of the neomycin-resistant gene. The mouse 3'-Cbl genomic fragment is inserted downstream of the neomycin-resistant gene. The arrangement of the inserts in the targeting vector are such that the 5'-Cbl and 3'-Cbl
10 arms of mouse homology are interrupted by the human Cbl gene and the neomycin-resistant gene, and this cassette is upstream of the thymidine kinase gene in the vector. The targeting vector is linearized, purified, and redissolved in TE (10mM Tris-HCl, pH 8, 1 mM EDTA), for electroporation.

15 A subclone of mouse strain 129 embryonic stem cell line, ESVJ (Go Germline, GenomeSystems, Inc.), is cultured on neomycin-resistant mouse fibroblast feeder layers and electroporated with 20 µg of the linearized targeting vector essentially as described by Koller, *et al.*, *Proc. Natl. Acad. Sci. USA* 88, 10730-10734, 1991. Stable
20 integrants are selected by positive-negative selection, using neomycin (G418-Geneticin; Invitrogen) at a final concentration of 200 µg/ml and 2 µM gancyclovir (FIAU, Moravsek Biochemicals, Brea, CA). After 10-12 days, the colonies are transferred into 96-well plates and tested for successful targeting and lack of rearrangement of the introduced human Cbl gene, by Southern blotting using conventional procedures.

25

Approximately 10-15 embryonic stem-targeted cells are injected into the blastocoe cavity of C57BL/6J embryos. Surviving blastocysts are transferred into the pseudopregnant CD-1 females. Animals chimeric by coat color are bred to C57BL/6J
30 animals to determine their germ line competency. Heterozygous mutants are identified by Southern blotting of DNA isolated from the tail, and brother-sister mating is carried out to generate homozygous knock-in mutant mouse lines expressing human c-Cbl.

Expression of dominant negative Cbl mutants in Cb^{+/+} mouse and human c-Cbl knock-in mouse

Because of the variation in adenoviral delivery to hindlimb muscles, it is preferred to employ an expression vector that permits quantitation of reporter gene expression e.g., the pAdTrack-CMV vector. Accordingly, the open reading frames encoding the dominant-negative mutants of human c-Cbl designated c-Cbl G306E (SEQ ID NO: 248), c-Cbl C381A (SEQ ID NO: 250), c-Cbl Y700F (SEQ ID NO: 252), c-Cbl Y731F (SEQ ID NO: 254), c-Cbl Y774F (SEQ ID NO: 256), c-Cbl 480 (SEQ ID NO: 260) and c-Cbl Y700F/Y731F/Y774F (SEQ ID NO: 258) as described in Example 5, are separately sub-cloned into the shuttle vector pAdTrack-CMV to permit their expression as a GFP fusion protein under the control of the CMV promoter. The GFP tag is not important to function of the Cbl protein moiety. The resultant plasmids are designated pAdTrack-CMV-G306E-GFP, pAdTrack-CMV-C381A-GFP, pAdTrack-CMV-Y700F-GFP, pAdTrack-CMV-Y731F-GFP, pAdTrack-CMV-Y774F-GFP, pAdTrack-CMV-Cbl 480-GFP, and pAdTrack-CMV-Y700F/Y731F/Y774F-GFP.

A further control plasmid comprising the full-length human c-Cbl open reading frame is also produced in the pAdTrack-CMV vector. This plasmid is designated pAdTrack-CMV-Cbl-GFP.

20

Adenoviruses comprising these constructs are produced essentially as described by He *et al.*, *Proc. Natl. Acad. Sci. USA.* 95: 2509-2514, 1998. Briefly, the pAdTrack-CMV-based vectors are linearized with *PmeI* and transfected into AdEasier-1 cells or *E. coli* BJ5183 cells carrying the pAdEasy-1 plasmid. The pAdEasy-1 adenoviral plasmid contains all Ad5 sequences except nucleotides 1-3,533 (encompassing the E1 genes) and nucleotides 28,130-30,820 (encompassing E3). Recombinant viral genomes are linearized with *PacI* and transfected into adenoviral packaging 293 cells in a six-well plate using lipofectamine 2000 (Invitrogen). Eight days after transfection, the recombinant virus is collected and subjected to one round of amplification in a T-25 flask with 1.5×10^6 293 cells, resulting in 2 ml of viral stocks.

Adenoviruses expressing the dominant negative c-Cbl mutants are introduced into both wild type mice and the c-Cbl knock-in mouse *supra*, essentially as described by Allamand *et al.*, *Gene Ther.* 7, 1385–1391, 2000. This is a robust system for the high efficiency (70-100%) transfer and expression of nucleic acid in mouse hindlimb skeletal muscle, wherein expression is maintained for >8 wk post infection, albeit being restricted to the muscle injected with the adenovirus. Briefly, mice (2-4 day old) are anesthetised via hypothermia and infectious adenovirus (2×10^9) containing shRNAs is injected in saline percutaneously into several muscles within the hindlimb. Pups are reintroduced to mothers and studied at 4-8 weeks of age. Relevant muscles are excised at different times after injection (1, 2, 4 and 8 weeks).

Expression of siRNAs and shRNAs in Cbl^{+/+} mouse and human c-Cbl knock-in mouse

Adenoviruses expressing the siRNAs and shRNAs as described in Example 5 are introduced into both wild type mice and the c-Cbl knock-in mouse *supra*, and mice are treated and analysed, essentially as described in the preceding paragraph.

Effect of dominant negative Cbl mutants, siRNAs and shRNAs on phenotypes of Cbl^{+/+} mouse and human c-Cbl knock-in mouse

The ability of inhibitory nucleic acids to mimic the phenotype of the Cbl^{+/+} mouse model is determined by their effect when administered to wild type (Cbl^{+/+} mice) and/or to mice in which the murine Cbl gene has been replaced with a human Cbl-encoding gene (i.e., the Cbl knock-in mouse). The latter murine model is particularly desirable for predicting effects on human c-Cbl in humans. Food intake, body weight, core temperature, oxygen consumption, *in vivo* glucose tolerance and whole body adiposity are determined for mice from one week of age.

A variety of parameters indicative of increased thermogenesis are also readily assessed in isolated hindlimb muscles using standard procedures, including mitochondrial size, number, and function, malonyl CoA levels as an index of the oxidation status of the mitochondria, intracellular triglyceride and glycogen levels.

Proton leak kinetics are determined on mitochondria isolated from the hindlimb muscles of mice treated with various nucleotide inhibitors. Mitochondria are isolated from muscle as previously described (St Pierre et al J. Biol. Chem. 278, 26597-26603, 2003). Leg muscle is removed from animals and homogenised in isolation buffer (100 mM KCl, 50 mM Tris, 2 mM EDTA, 0.5% BSA, pH 7.4 at 4 C. The homogenate is centrifuged at 2000 x g for 5 min. The supernatant is centrifuged at 10,000 x g for 10 min. The pellet from this spin is washed and resuspended in isolation buffer. Oxygen consumption rates are measured using Clark type electrode and the membrane potential is measured using a TPMP electrode. Rotenone (5 μ M), oligomycin (1 μ g/mg mitochondrial protein) and nigericin (80 ng/ml) are added at the start of the assay. TPMP will be added to 1.3 μ M for calibration. Mitochondria are fed 94 mM succinate and the inhibitor malonate is then added gradually up to 1.3 mM to inhibit mitochondrial respiration and membrane potential. Finally, p-trifluoromethoxyphenylhydraz one (0.15 μ M) is added to determine drift in the TPMP electrode. To determine that this effect is specific to muscle, similar studies are performed using mitochondria isolated from other tissues.

Results

Wild-type mice, and Cbl knock-in mice transfected with adenovirus expressing full-length native human c-Cbl in the sense orientation, have normal phenotypes with respect to fat deposition, metabolism and metabolic rate in hindlimb muscles. These animals also provide a normal baseline of mitochondrial function and thermogenic activity, as determined by the proton leak kinetics of cells from isolated hindlimb muscles. In marked contrast, those animals administered with adenovirus expressing the dominant-negative mutant constructs pBabe-Cbl G306E, pBabe-C381A, pBabe-Cbl Y700F, pBabe-Cbl Y731F, or pBabe-Y774F exhibit muscle phenotypes that partially or completely mimic the lean muscle phenotype of the Cbl^{-/-} mouse as described in Examples 1-4. Additionally, proton leak kinetics of cells from isolated hindlimb muscles of these animals are consistent with enhanced mitochondrial respiration rates compared to control animals.

Such data suggest that the effects of inhibitors of c-Cbl expression can be assayed or validated by expressing the nucleic acid inhibitors in the hindlimb muscles of a suitable mouse model and determining the level of fat, glucose uptake, glucose transport into fat and/or muscle, muscle temperature, and resting metabolic rate, of hindlimb muscles from the animals. Additionally, proton leak kinetics of hindlimb muscles also provide a means of assessing efficacy of inhibitory molecules.

Proceeding on this basis, the level of fat, glucose uptake, glucose transport into fat and/or muscle, muscle temperature, and resting metabolic rate of hindlimb muscles from animals administered with adenovirus expressing c-Cbl antisense RNA or the dominant negative mutant c-Cbl Y700F/Y731F/Y774F. Proton leak kinetics are also determined for hindlimb muscle cells. Reduced fat mass and/or increased glucose transport into fat or muscle and/or increased muscle temperature and/or increased mitochondrial respiration rate of hindlimb muscles expressing these molecules, relative to the levels of these parameters for animals administered with adenovirus expressing the full-length c-Cbl open reading frame in the sense orientation, indicate that these molecules are also effective antagonists of c-Cbl expression.

Adenovirus (Ad5) expressing a series of shRNAs designed against human c-Cbl expression (Table 4) is also tested in this animal model, to determine *in vivo* efficacy against the human Cbl gene. Reduced fat mass and/or increased temperature and/or increased glucose transport into fat or muscle and/or increased muscle temperature and/or increased mitochondrial respiration rate of hindlimb muscles expressing these molecules, relative to the levels of these parameters for animals administered with adenovirus expressing the full-length c-Cbl open reading frame in the sense orientation, indicate that these molecules are also effective antagonists of c-Cbl expression.

Molecules that produce one or more of these desired effects in animal models are entered into clinical trials.

EXAMPLE 9

Assays for mitochondrial function

Expression vectors and cell lines

C2C12 cells (ATCC CRL-1772; Yaffe *et al.*, *Nature* 270, 725-727, 1977; Yaffe
5 *et al.*, *Differentiation* 7, 159-166, 1977) are obtained, maintained, and modified to
express human c-Cbl and dominant negative c-Cbl mutants, antisense molecules,
siRNAs and shRNAs as described in example 6.

Electron microscopy

To determine the effects of c-Cbl deletion on mitochondrial structure and
10 function, C2C12 cells expressing dominant negative mutants, shRNA or siRNA are
fixed with 2.5% glutaraldehyde, 1% paraformaldehyde and 0.03% picric acid in 0.1 M
sodium cacodylate buffer pH 7.4, washed in 0.1 M cacodylate buffer, postfixed with
1% osmiumtetroxide/1.5% potassium ferrocyanide for 1 h, washed in water and
15 stained with 1 % uranyl acetate for 30 min followed by rehydration in alcohol. Samples
are embedded in epon and 60 nm sections will be cut using an ultramicrotome.
Mitochondrial volume density and cristae surface density of cells is measured as
described by [Wiebel (1979) Stereological methods: Practical methods for Biological
morphometry, Academic press, London].

20 *Levels of Mitochondrial proteins*

The levels of a range of mitochondrial proteins (cytochrome C, ATP synthase,
UCP2, UCP3, PGC1 as well as a range of enzymes involved in metabolism of reactive
oxygen species (ROS)) is determined readily by western blotting.

25 One hypothesis to explain our observations is that c-Cbl may control the
production of reactive oxygen species (ROS). This is likely as tyrosine kinase GF
receptors like the EGFR control the production of H₂O₂. Because in a c-Cbl null
background the level of these receptors will be increased it is quite likely that the level
of ROS will also be elevated. ROS has previously been shown to activate
30 mitochondrial uncoupling proteins in a FFA-dependent manner (Echtay, Roussel, St
Pierre *et al* *Nature* 2001). To test this hypothesis, the level of ROS in c-Cbl^{-/-} mice as
well as in C2C12 cells depleted of c-Cbl, using the methods described by Arsenijevic
et al *Nature Genetics* 26, 435-439, 2000.

We Claim:

1. A method of identifying a compound that is capable of modulating feeding behavior, fat deposition, metabolic rate, or the ratio of lean muscle mass to body fat in a subject, said method comprising performing an assay to measure
5 a metabolism-associated phenotype that has been determined for a genetically modified non-human animal that comprises a genetic modification within an allele of its Cbl locus wherein said genetic modification reduces or prevents expression of a functional endogenous Cbl in said animal, and wherein said assay is conducted in the presence and absence of a compound to be tested;
10 and determining the effect of the compound on the phenotype wherein a modified phenotype indicates that the compound is capable of modulating feeding behavior, fat deposition, metabolic rate, or the ratio of lean muscle mass to body fat in a subject.
- 15 2. The method according to claim 1 wherein the assay to determine a metabolism-associated phenotype measures Cbl-mediated ubiquitination of the insulin receptor in the presence and absence of the compound.
3. The method according to claim 2 wherein the assay comprises:
20 (a) providing a cell that is capable of effecting the c-Cbl-mediated ubiquitination of the insulin receptor;
(b) incubating the cell in the presence and absence of a compound to be tested; and
(c) determining c-Cbl-mediated ubiquitination of the insulin receptor in the
25 presence and absence of the compound wherein a modified level of c-Cbl-mediated ubiquitination of the insulin receptor indicates that the compound is capable of modulating feeding behavior, fat deposition, metabolic rate, or the ratio of lean muscle mass to body fat in a subject.
- 30 4. The method according to claim 3 wherein the compound reduces or inhibits Cbl-mediated ubiquitination of the insulin receptor thereby indicating that said compound is capable of enhancing feeding behavior in a subject.

5. The method according to claim 3 wherein the compound reduces or inhibits Cbl-mediated ubiquitination of the insulin receptor thereby indicating that said compound is capable of reducing fat deposition in a subject.
- 5 6. The method according to claim 3 wherein the compound reduces or inhibits Cbl-mediated ubiquitination of the insulin receptor thereby indicating that said compound is capable of enhancing metabolic rate in a subject.
- 10 7. The method according to claim 3 wherein the compound reduces or inhibits Cbl-mediated ubiquitination of the insulin receptor thereby indicating that said compound is capable of enhancing the ratio of lean muscle mass to body fat in a subject.
- 15 8. The method according to claim 3 wherein the compound enhances or agonizes Cbl-mediated ubiquitination of the insulin receptor thereby indicating that said compound is capable of reducing feeding behavior and/or enhancing fat deposition in a subject and/or reducing metabolic rate in a subject and/or reducing the ratio of lean muscle mass to body fat in a subject.
- 20 9. The method according to claim 3 comprising performing an immunoassay wherein the level of c-Cbl-mediated ubiquitination of the insulin receptor is determined by contacting the insulin receptor with an antibody that binds to ubiquitin under conditions sufficient for an antigen-antibody complex to form and detecting the antibody bound to the receptor.
- 25 10. The method according to claim 9 further comprising contacting the insulin receptor with an antibody that binds to the insulin receptor under conditions sufficient for an antigen-antibody complex to form.
- 30 11. The method according to claim 3 comprising performing an immunoassay by a process comprising:
 - (a) providing a cell that is capable of effecting the c-Cbl-mediated ubiquitination of the insulin receptor;
 - (b) incubating the cell in the presence and absence of a compound to be tested;

- (c) contacting an extract of the cell comprising the insulin receptor with an antibody that binds to the insulin receptor under conditions sufficient for an antigen-antibody complex to form thereby capturing the insulin receptor;
- (d) contacting the captured insulin receptor with an antibody that binds to ubiquitin under conditions sufficient for an antigen-antibody complex to form; and
- (e) detecting the antibody bound at (d).

12. The method according to claim 11 wherein the antibody bound at (d) is detected by contacting the antibody with a tertiary antibody that is capable of producing a detectable signal.

13. The method according to claim 1 wherein the assay to determine a metabolism-associated phenotype measures phosphorylation of a tyrosine residue on Cbl protein in the presence and absence of the compound.

14. The method according to claim 1 wherein the assay to determine a metabolism-associated phenotype measures the amount of Cbl protein in the cell in the presence and absence of the compound.

15. The method according to claim 14 wherein the assay comprises:

- (a) providing a cell that is capable of expressing c-Cbl protein;
- (b) incubating the cell in the presence and absence of a compound to be tested; and
- (c) determining amount of c-Cbl protein in the cell in the presence and absence of the compound wherein a modified level of c-Cbl protein indicates that the compound is capable of modulating feeding behavior, fat deposition, metabolic rate, or the ratio of lean muscle mass to body fat in a subject.

16. The method according to claim 15 wherein the compound reduces or inhibits Cbl expression as determined by a reduced amount of Cbl protein in the cell thereby indicating that said compound is capable of enhancing feeding behavior in a subject.

17. The method according to claim 15 wherein the compound reduces or inhibits Cbl expression as determined by a reduced amount of Cbl protein in the cell thereby indicating that said compound is capable of reducing fat deposition in a subject.

5

18. The method according to claim 15 wherein the compound reduces or inhibits Cbl expression as determined by a reduced amount of Cbl protein in the cell thereby indicating that said compound is capable of enhancing metabolic rate in a subject.

10

19. The method according to claim 15 wherein the compound reduces or inhibits Cbl expression as determined by a reduced amount of Cbl protein in the cell thereby indicating that said compound is capable of enhancing the ratio of lean muscle mass to body fat in a subject.

15

20. The method according to claim 15 wherein the compound enhances or agonizes Cbl expression as determined by an increased amount of Cbl protein in the cell thereby indicating that said compound is capable of reducing feeding behavior and/or enhancing fat deposition in a subject and/or reducing metabolic rate in a subject and/or reducing the ratio of lean muscle mass to body fat in a subject.

20

21. The method according to claim 15 comprising performing an immunoassay wherein the amount of c-Cbl is determined by contacting the Cbl protein with an antibody that binds to Cbl under conditions sufficient for an antigen-antibody complex to form and detecting the antibody bound to the Cbl protein.

25

22. The method according to claim 21 wherein the antibody bound to the Cbl protein is detected by contacting the antibody with a secondary antibody that is capable of producing a detectable signal.

30

23. The method according to claim 15 comprising performing an immunoassay wherein the amount of c-Cbl is determined by contacting the Cbl protein with a primary and secondary antibody that each bind to Cbl under conditions

sufficient for antigen-antibody complexes to form and detecting an antibody bound to the Cbl protein.

24. The method according to claim 23 wherein the antibody bound to the Cbl protein is detected by contacting the antibody with a secondary antibody that is capable of producing a detectable signal.
25. The method according to claim 23 wherein the primary and secondary antibody bind to different epitopes on the Cbl protein.
26. The method according to claim 15 comprising performing an immunoassay by a process comprising:
- (a) providing a cell that is capable of expressing c-Cbl protein;
 - (b) incubating the cell in the presence and absence of a compound to be tested;
 - (c) contacting an extract of the cell comprising the Cbl protein with an antibody that binds to Cbl protein under conditions sufficient for an antigen-antibody complex to form thereby capturing the Cbl protein; and
 - (d) detecting the antibody bound at (e).
27. The method according to claim 15 comprising performing an immunoassay by a process comprising:
- (a) providing a cell that is capable of expressing c-Cbl protein;
 - (b) incubating the cell in the presence and absence of a compound to be tested;
 - (c) contacting an extract of the cell comprising the Cbl protein with an antibody that binds to Cbl protein under conditions sufficient for an antigen-antibody complex to form thereby capturing the Cbl protein;
 - (d) contacting the captured Cbl protein with an antibody that binds to Cbl protein under conditions sufficient for an antigen-antibody complex to form, wherein said antibody binds to a different epitope on Cbl to the antibody at (c); and
 - (e) detecting the antibody bound at (d).
28. The method according to claim 26 or 27 wherein the antibody is detected by contacting the antibody with an antibody that is capable of producing a detectable signal.

29. The method according to claim 1 wherein the assay to determine a metabolism-associated phenotype measures Cbl-mediated fat and/or glucose metabolism in the cell in the presence and absence of the compound.
- 5 30. The method according to claim 29 wherein the assay to determine a metabolism-associated phenotype measures a phenotype in the presence and absence of the compound selected from the group consisting of fat mass, glucose transport, muscle thermogenesis, mitochondrial structure, mitochondrial function, and mitochondrial respiration rate.
- 10 31. The method according to claim 29 or 30 wherein the assay measures muscle thermogenesis in the cell in the presence and absence of the compound.
- 15 32. The method according to claim 31 wherein muscle thermogenesis in the presence and absence of the compound is determined by a process comprising determining the proton leak kinetics of a cell in the presence and absence of the compound.
- 20 33. The method according to claim 32 comprising:
- (a) providing a cell of myoblast lineage capable of expressing c-Cbl protein;
 - (b) incubating the cell in the presence and absence of a compound to be tested; and
 - (c) determining the respiration rate and/or membrane potential of the cell in the presence and absence of the compound wherein a modified respiration rate and/or membrane potential indicates that the compound is capable of modulating feeding behavior, fat deposition, metabolic rate, or the ratio of lean muscle mass to body fat in a subject.
- 25 34. The method according to claim 33 wherein the compound enhances respiration rate and/or membrane potential of the cell thereby indicating that said compound is capable of enhancing feeding behavior in a subject.
- 30

35. The method according to claim 33 wherein the compound enhances respiration rate and/or membrane potential of the cell thereby indicating that said compound is capable of reducing fat deposition in a subject.

5 36. The method according to claim 33 wherein the compound enhances respiration rate and/or membrane potential of the cell thereby indicating that said compound is capable of enhancing metabolic rate in a subject.

10 37. The method according to claim 33 wherein the compound enhances respiration rate and/or membrane potential of the cell thereby indicating that said compound is capable of enhancing the ratio of lean muscle mass to body fat in a subject.

15 38. The method according to claim 33 wherein the compound reduces or inhibits respiration rate and/or membrane potential of the cell thereby indicating that said compound is capable of reducing feeding behavior and/or enhancing fat deposition in a subject and/or reducing metabolic rate in a subject and/or reducing the ratio of lean muscle mass to body fat in a subject.

20 39. The method according to claim 29 or 30 wherein the assay comprises:
(a) providing a compound to be tested to an animal subject that expresses a functional Cbl protein; and
(b) determining a metabolism-associated phenotype in a cell or tissue of the animal wherein a modified phenotype in the presence of the compound
25 indicates that the compound is capable of modulating feeding behavior, fat deposition, metabolic rate, or the ratio of lean muscle mass to body fat in a subject.

30 40. The method according to claim 39 wherein the metabolism-associated phenotype is selected from the group consisting of fat mass, glucose transport, muscle thermogenesis, mitochondrial structure, mitochondrial function, and mitochondrial respiration rate.

41. The method according to claim 40 wherein the metabolism-associated phenotype is muscle thermogenesis.

5 42. The method according to claim 41 wherein muscle thermogenesis in the presence of the compound is determined by a process comprising determining the proton leak kinetics of a cell or tissue of the animal.

10 43. The method according to claim 41 or 42 wherein muscle thermogenesis is determined by measuring the respiration rate and/or membrane potential of a cell from the animal wherein a modified respiration rate and/or membrane potential indicates that the compound is capable of modulating feeding behavior, fat deposition, metabolic rate, or the ratio of lean muscle mass to body fat in a subject.

15 44. The method according to claim 43 wherein the compound enhances respiration rate and/or membrane potential of the cell thereby indicating that said compound is capable of enhancing feeding behavior in a subject.

20 45. The method according to claim 43 wherein the compound enhances respiration rate and/or membrane potential of the cell thereby indicating that said compound is capable of reducing fat deposition in a subject.

25 46. The method according to claim 43 wherein the compound enhances respiration rate and/or membrane potential of the cell thereby indicating that said compound is capable of enhancing metabolic rate in a subject.

30 47. The method according to claim 43 wherein the compound enhances respiration rate and/or membrane potential of the cell thereby indicating that said compound is capable of enhancing the ratio of lean muscle mass to body fat in a subject.

48. The method according to claim 43 wherein the compound reduces or inhibits respiration rate and/or membrane potential of the cell thereby indicating that said compound is capable of reducing feeding behavior and/or enhancing fat

deposition in a subject and/or reducing metabolic rate in a subject and/or reducing the ratio of lean muscle mass to body fat in a subject.

- 5 49. The method according to claim 39 wherein the animal subject is a non-human animal subject.
50. The method according to claim 49 wherein the non-human animal subject expresses an endogenous native Cbl protein.
- 10 51. The method according to claim 49 wherein the non-human animal subject expresses an introduced human Cbl protein.
52. The method according to claim 49 wherein the non-human animal is a mammal.
- 15 53. The method according to claim 52 wherein the mammal is selected from the group consisting of rodent, dog, pig, bovine, sheep, horse and goat.
54. The method according to claim 53 wherein the rodent is selected from the group consisting of rabbit, rat, guinea pig and mouse.
- 20 55. The method according to claim 54 wherein the rodent is a mouse.
56. The method according to claim 39 wherein the compound is administered to muscle tissue of the animal subject.
- 25 57. The method according to claim 56 wherein the metabolism-associated phenotype is determined in muscle tissue of the animal subject.
- 30 58. The method according to claim 1 comprising comparing the effect of the compound on the metabolism-associated phenotype to a metabolism-associated phenotype for a genetically modified non-human animal that comprises a genetic modification within an allele of its Cbl locus wherein said genetic modification reduces or prevents expression of a functional

endogenous Cbl in said animal, and wherein the ability of the compound to mimic or reproduce the phenotype of the genetically modified non-human animal indicates that the compound is capable of enhancing feeding behavior and/or reducing fat deposition and/or enhancing metabolic rate and/or enhancing the ratio of lean muscle mass to body fat in a subject.

59. The method according to claim 1 comprising comparing the effect of the compound on the metabolism-associated phenotype to a metabolism-associated phenotype for a non-human animal that expresses a functional Cbl protein, and wherein the ability of the compound to mimic or reproduce the phenotype of the non-human animal indicates that the compound is capable of reducing feeding behavior and/or enhancing fat deposition and/or reducing metabolic rate and/or reducing the ratio of lean muscle mass to body fat in a subject.

60. A method of identifying a compound that suppresses or reduces feeding behavior, said method comprising:

- (a) administering a compound to a genetically modified non-human animal comprising a genetic modification within an allele of its Cbl locus wherein said genetic modification reduces or prevents expression of a functional endogenous Cbl in said animal; and
- (b) determining the feeding behavior of the animal, wherein reduced appetite or dietary intake of the animal compared to the appetite or dietary intake of a Cbl-deficient animal to which the compound has not been administered indicates that the compound suppresses or reduces feeding behavior.

61. A method for identifying a compound that suppresses or reduces feeding behavior, said method comprising determining the ubiquitin ligase activity of a Cbl protein in the presence and absence of the compound wherein enhanced ubiquitin ligase activity of the Cbl protein in the presence of the compound indicates that the compound suppresses or reduces feeding behavior.

62. A method for identifying a compound that suppresses or reduces feeding behavior comprising determining the level of tyrosine phosphorylation of a Cbl

protein in the presence and absence of the compound wherein enhanced phosphorylation of tyrosine residues in the Cbl protein in the presence of the compound indicates that the compound suppresses or reduces feeding behavior.

5

63. A method of identifying a compound that enhances feeding behavior said method comprising:

(a) administering a compound that suppresses appetite or dietary intake to a genetically modified non-human animal comprising a genetic modification within an allele of its Cbl locus wherein said genetic modification reduces or prevents expression of a functional endogenous Cbl in said animal and determining the feeding behavior of the animal;

10

(b) administering a compound to the animal and determining the feeding behavior of the animal, wherein enhanced appetite or dietary intake at (b) compared to (a) indicates that the compound enhances feeding behavior.

15

64. A method of identifying a compound that enhances feeding behavior comprising determining the ubiquitin ligase activity of a Cbl protein in the presence and absence of the compound wherein reduced ubiquitin ligase activity of the Cbl protein in the presence of the compound indicates that the compound enhances feeding behavior.

20

65. A method for identifying a compound that enhances feeding behavior comprising determining the level of tyrosine phosphorylation of a Cbl protein in the presence and absence of the compound wherein reduced phosphorylation of tyrosine residues in the Cbl protein in the presence of the compound indicates that the compound enhances feeding behavior.

25

66. A method of identifying a compound that modulates feeding behavior, said method comprising:

30

(a) administering a compound to a non-human animal expressing a functional Cbl protein and determining the feeding behavior of the animal;

(b) determining the feeding behavior of a genetically modified non-human animal comprising a genetic modification within an allele of its Cbl locus wherein said

genetic modification reduces or prevents expression of a functional endogenous Cbl in said animal; and

- (c) comparing the feeding behavior of the animals at (a) and (b) wherein a comparable feeding behavior between (a) and (b) indicates that the compound modulates feeding behavior.

67. A method of identifying a compound that modulates feeding behavior comprising determining the ubiquitin ligase activity of a Cbl protein in the presence and absence of the compound wherein modified ubiquitin ligase activity of the Cbl protein in the presence of the compound indicates that the compound enhances feeding behavior.

68. A method for identifying a compound that modulates feeding behavior comprising determining the level of tyrosine phosphorylation of a Cbl protein in the presence and absence of the compound wherein modified phosphorylation of tyrosine residues in the Cbl protein in the presence of the compound indicates that the compound modulates feeding behavior.

69. A method of identifying a compound that enhances fat deposition or reduces lean muscle mass or enhances the ratio of body fat to muscle or reduces metabolic rate, said method comprising:

- (a) administering a compound to a genetically modified non-human animal comprising a genetic modification within an allele of its Cbl locus wherein said genetic modification reduces or prevents expression of a functional endogenous Cbl in said animal; and
- (b) determining the fat content of the animal, wherein enhanced fat content of the animal compared to the fat content of a Cbl-deficient animal to which the compound has not been administered indicates that the compound enhances fat deposition or reduces lean muscle mass or enhances the ratio of body fat to muscle or reduces metabolic rate.

70. A method of identifying a compound that enhances fat deposition or reduces lean muscle mass or enhances the ratio of body fat to muscle or reduces metabolic rate comprising determining the ubiquitin ligase activity of a Cbl

protein in the presence and absence of the compound wherein enhanced ubiquitin ligase activity of the Cbl protein in the presence of the compound indicates that the compound enhances fat deposition or reduces lean muscle mass or enhances the ratio of body fat to muscle or reduces metabolic rate.

5

71. A method for identifying a compound that enhances fat deposition or reduces lean muscle mass or enhances the ratio of body fat to muscle or reduces metabolic rate comprising determining the level of tyrosine phosphorylation of a Cbl protein in the presence and absence of the compound wherein enhanced phosphorylation of tyrosine residues in the Cbl protein in the presence of the compound indicates that the compound enhances fat deposition or reduces lean muscle mass or enhances the ratio of body fat to muscle or reduces metabolic rate.

10

- 15 72. A method of identifying a compound that reduces fat deposition or enhances lean muscle mass or reduces the ratio of body fat to muscle or enhances metabolic rate, said method comprising:

- (a) administering a compound that enhances fat deposition or glucose uptake to a genetically modified non-human animal comprising a genetic modification within an allele of its Cbl locus wherein said genetic modification reduces or prevents expression of a functional endogenous Cbl in said animal and determining the fat content of the animal; and
- (b) administering a compound to the animal and determining the fat content of the animal, wherein a similar or reduced fat content at (b) compared to (a) indicates that the compound reduces fat deposition or enhances lean muscle mass or reduces the ratio of body fat to muscle or enhances metabolic rate.

20

25

73. A method of identifying a compound that reduces fat deposition or enhances lean muscle mass or reduces the ratio of body fat to muscle or enhances metabolic rate comprising:

30

- (a) administering a compound to a non-human animal expressing a functional Cbl protein and determining the fat content of the animal;
- (b) determining the fat content of a genetically modified non-human animal comprising a genetic modification within an allele of its Cbl locus wherein said

genetic modification reduces or prevents expression of a functional endogenous Cbl in said animal; and

- (c) comparing the fat contents of the animals at (a) and (b) wherein a comparable fat content between (a) and (b) indicates that the compound reduces fat deposition or enhances lean muscle mass or reduces the ratio of body fat to muscle or enhances metabolic rate.

74. A method of identifying a compound that reduces fat deposition or enhances lean muscle mass or reduces the ratio of body fat to muscle or enhances metabolic rate comprising determining the ubiquitin ligase activity of a Cbl protein in the presence and absence of the compound wherein reduced ubiquitin ligase activity of the Cbl protein in the presence of the compound indicates that the compound reduces fat deposition or enhances lean muscle mass or reduces the ratio of body fat to muscle or enhances metabolic rate.

75. A method for identifying a compound that reduces fat deposition or enhances lean muscle mass or reduces the ratio of body fat to muscle or enhances metabolic rate comprising determining the level of tyrosine phosphorylation of a Cbl protein in the presence and absence of the compound wherein reduced phosphorylation of tyrosine residues in the Cbl protein in the presence of the compound indicates that the compound reduces fat deposition or enhances lean muscle mass or reduces the ratio of body fat to muscle or enhances metabolic rate.

76. A method of identifying a compound that enhances glucose uptake, said method comprising:

- (a) administering a compound to a genetically modified non-human animal comprising a genetic modification within an allele of its Cbl locus wherein said genetic modification reduces or prevents expression of a functional endogenous Cbl in said animal; and
- (b) determining the glucose uptake into liver, fat or muscle cells of the animal, wherein enhanced uptake compared to the glucose uptake into liver, fat or muscle cells of a Cbl-deficient animal to which the compound has not been administered indicates that the compound enhances glucose uptake.

77. A method of identifying a compound that enhances glucose uptake comprising determining the ubiquitin ligase activity of a Cbl protein in the presence and absence of the compound wherein reduced ubiquitin ligase activity of the Cbl protein in the presence of the compound indicates that the compound reduces fat deposition or enhances glucose uptake.

78. A method for identifying a compound that enhances glucose uptake comprising determining the level of tyrosine phosphorylation of a Cbl protein in the presence and absence of the compound wherein reduced phosphorylation of tyrosine residues in the Cbl protein in the presence of the compound indicates that the compound enhances glucose uptake.

79. A method of identifying a compound that reduces glucose uptake into liver, fat or muscle cells, said method comprising:

(a) administering a compound that enhances glucose uptake to a genetically modified non-human animal comprising a genetic modification within an allele of its Cbl locus wherein said genetic modification reduces or prevents expression of a functional endogenous Cbl in said animal and determining the glucose uptake into liver, fat or muscle cells;

(b) administering a compound to the animal and determining the glucose uptake into liver, fat or muscle cells of the animal, wherein a similar or reduced uptake at (b) compared to (a) indicates that the compound reduces glucose uptake into liver, fat or muscle cells.

80. A method of identifying a compound that reduces glucose uptake into liver, fat or muscle cells comprising:

(a) administering a compound to a non-human animal expressing a functional Cbl protein and determining the glucose uptake into liver, fat or muscle cells of the animal;

(b) determining the glucose uptake into liver, fat or muscle cells of a genetically modified non-human animal comprising a genetic modification within an allele of its Cbl locus wherein said genetic modification reduces or prevents expression of a functional endogenous Cbl in said animal; and

- (c) comparing the glucose uptake into liver, fat or muscle cells of the animals at (a) and (b) wherein a comparable uptake between (a) and (b) indicates that the compound reduces glucose uptake into liver, fat or muscle cells.

5 81. A method of identifying a compound that reduces glucose uptake comprising determining the ubiquitin ligase activity of a Cbl protein in the presence and absence of the compound wherein enhanced ubiquitin ligase activity of the Cbl protein in the presence of the compound indicates that the compound reduces glucose uptake.

10

82. A method for identifying a compound that reduces glucose uptake comprising determining the level of tyrosine phosphorylation of a Cbl protein in the presence and absence of the compound wherein enhanced phosphorylation of tyrosine residues in the Cbl protein in the presence of the compound indicates that the compound reduces glucose uptake.

15

83. The method according to any one of claims 1 to 82 wherein the compound being tested is a protein.

20 84. The method according to claim 83 wherein the protein is a dominant negative mutant of Cbl.

85. The method according to claim 84 wherein the dominant negative mutant of Cbl comprises an amino acid sequence selected from the group consisting of
25 SEQ ID NO: 248, SEQ ID NO: 250, SEQ ID NO: 252, SEQ ID NO: 254, SEQ ID NO: 256, SEQ ID NO: 258 and SEQ ID NO: 260.

84. The method according to any one of claims 1 to 83 wherein the compound being tested is nucleic acid.

30

85. The method according to claim 84 wherein the nucleic acid comprises an antisense molecule, ribozyme, siRNA, or shRNA.

86. The method according to claim 85 wherein the nucleic acid comprises siRNA, or shRNA that comprises a nucleotide sequence set forth in any one of SEQ ID NOS: 4-239.
- 5 87. The method according to any one of claims 1 to 83 wherein the compound tested is a small organic molecule.
88. The method according to any one of claims 1 to 83 wherein the compound in an antibody that binds to a Cbl protein.
- 10 89. The method according to any one of claims 1 to 88 further comprising formulating the identified compound for administration to a non-human animal or a human.
- 15 90. The method according to any one of claims 1 to 89 further comprising producing or synthesizing the compound.
91. A process for identifying or determining a compound that modulates feeding behavior, fat deposition, metabolic rate, or the ratio of lean muscle mass to body fat in a subject, said process comprising:
- 20 (a) performing the method according to any one of claims 1 to 90;
- (b) optionally, determining the structure of the compound; and
- (c) providing the compound or the name or structure of the compound.
- 25 92. The process according to claim 91 wherein the compound name or structure is provided in a paper form, machine-readable form, or computer-readable form.
93. The process according to claim 90 or 91 wherein the compound structure is known.
- 30 94. The process according to any one of claims 90 to 92 wherein the compound or the name or structure of the compound is provided with an indication as to its use.

95. A process for producing a compound that modulates feeding behavior, fat deposition, metabolic rate, or the ratio of lean muscle mass to body fat in a subject, said process comprising:

- (a) performing the method according to any one of claims 1 to 90 to thereby identify or determine a compound;
- (b) optionally, determining the structure of the compound or modulator;
- (c) optionally, providing the name or structure of the compound or modulator; and
- (d) producing the compound or modulator.

96. The process according to claim 95 wherein the compound name or structure is provided in a paper form, machine-readable form, or computer-readable form.

97. The process according to claim 95 or 96 wherein the compound or the name or structure of the compound is provided with an indication as to its use.

98. The process according to claim 97 further comprising formulating the compound in a suitable diluent or excipient.

99. Use of an isolated siRNA or shRNA comprising a nucleotide sequence set forth in any one of SEQ ID Nos: 4-239 to modulate a metabolism-associated phenotype in a cell, tissue or animal subject.

100. Use of a isolated nucleic acid molecule comprising a nucleotide sequence set forth in any one of SEQ ID Nos: 247, 249, 252, 253, 255, 257, or 259 to produce a dominant negative inhibitor molecule capable of modulating a metabolism-associated phenotype in a cell, tissue or animal subject.

101. Use according to claim 99 or 100 wherein the modulation to a metabolism-associated phenotype is selected from the group consisting of:

- (a) inhibition or decrease of Cbl-mediated ubiquitination of an insulin receptor;
- (b) inhibition or decrease in Cbl protein level; and
- (c) enhanced muscle thermogenesis.

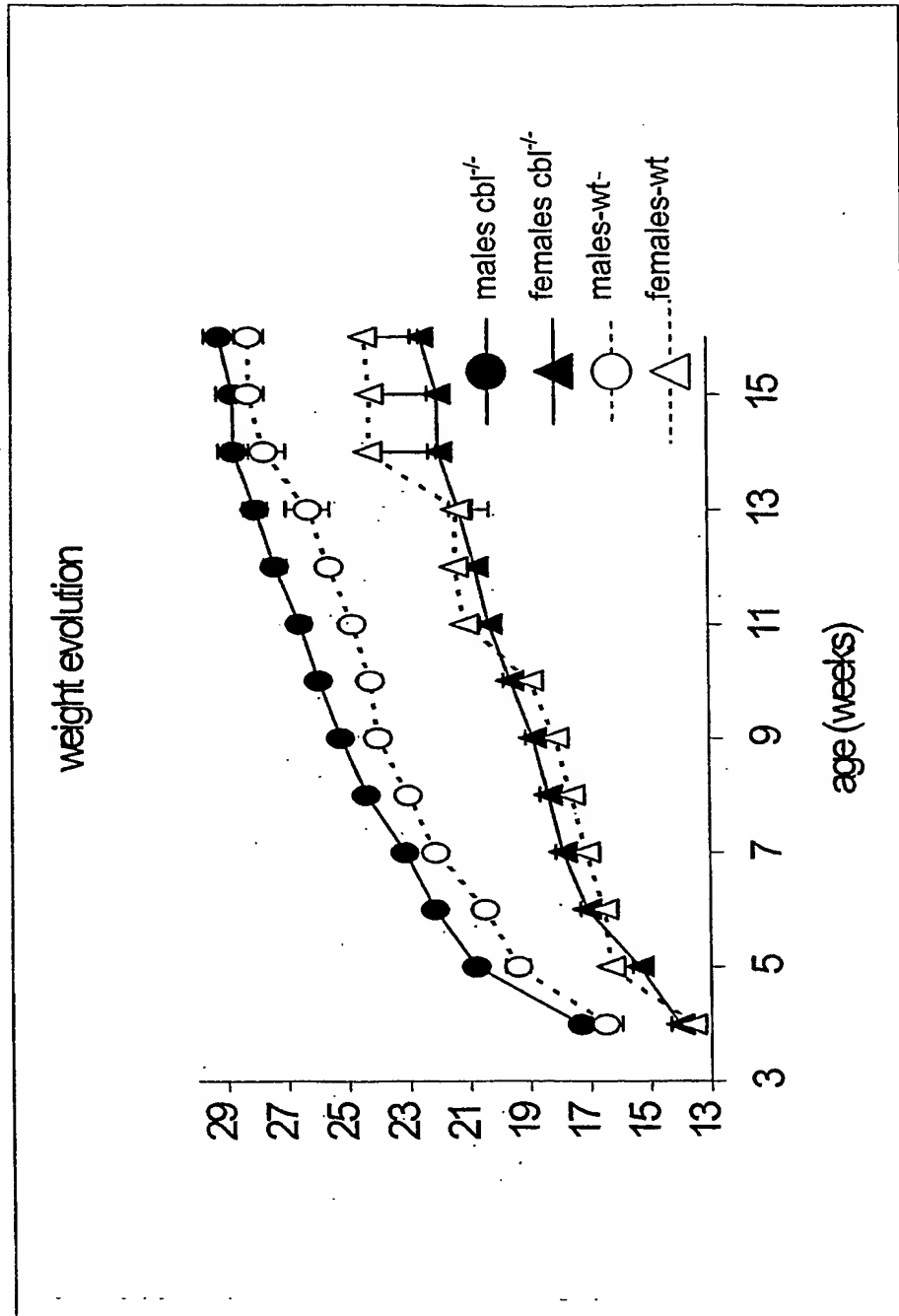


FIGURE 1

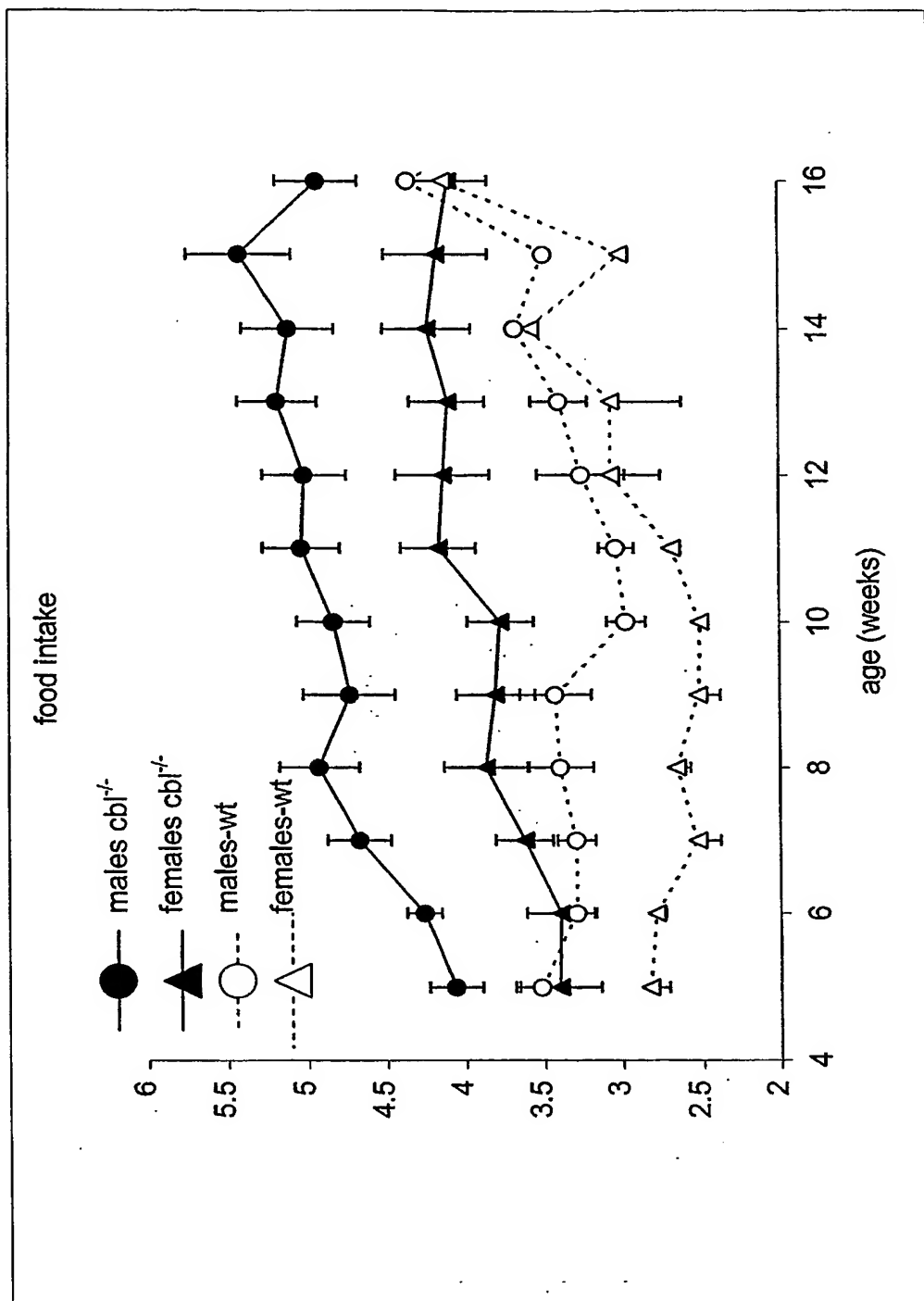


FIGURE 2

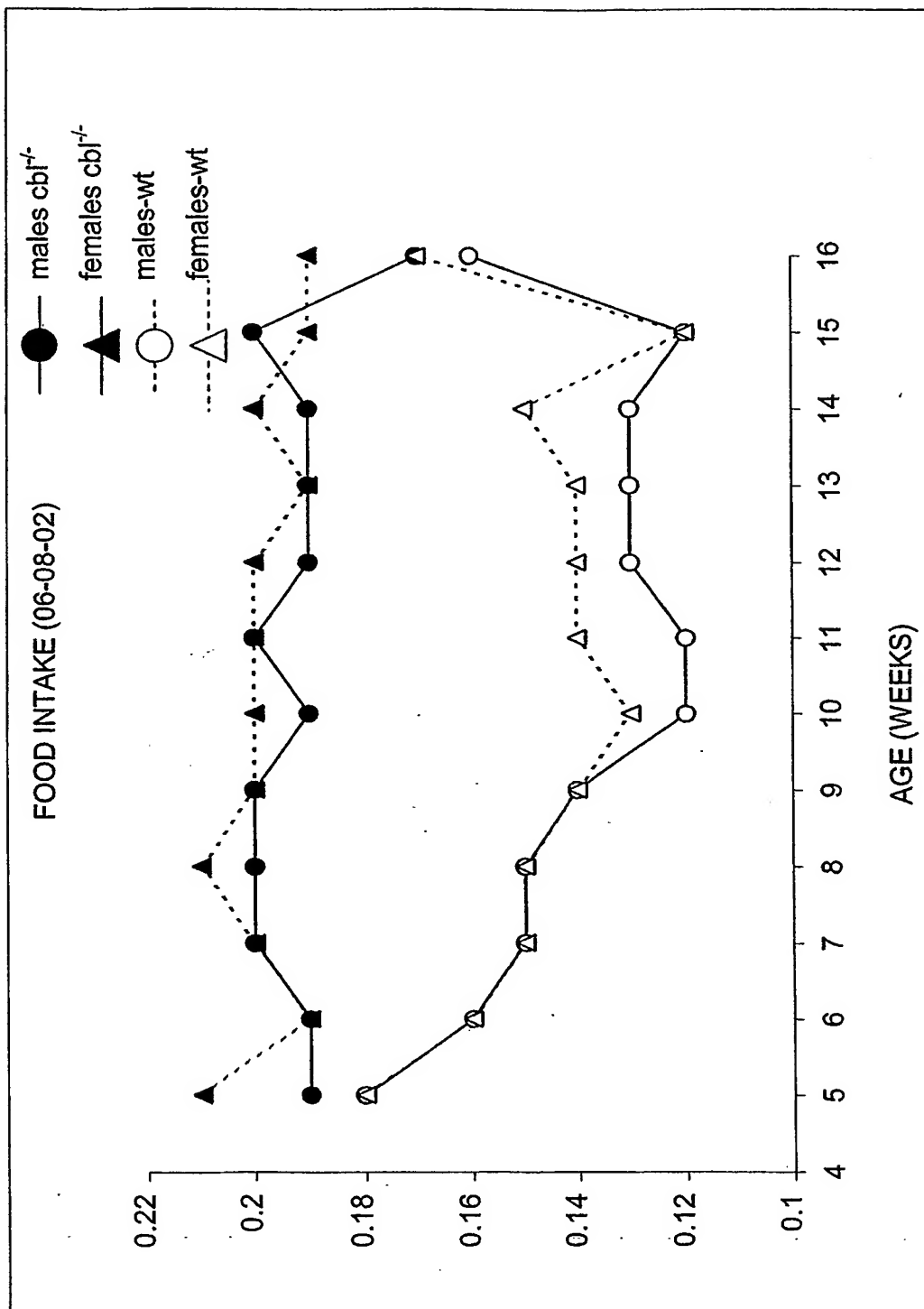


FIGURE 3

TISSUE WEIGHT

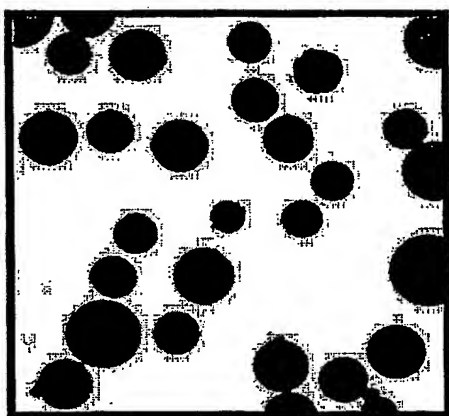
Wild Type

AVG	30.4	0.543	0.141	0.204	100	1.79	0.46	0.67
SEM	0.54	0.129	0.002	0.011		0.46	0.01	0.02
	BW	WAT	BAT	QUAD	BW	WAT	BAT	QUAD

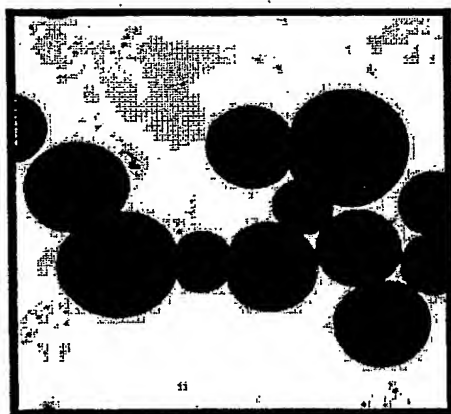
Cbl-deficient

AVG	30.00	0.226	0.073	0.206	100.00	0.75	0.24	0.69
SEM	0.95	0.021	0.005	0.013		0.07	0.01	0.04
	BW	WAT	BAT	QUAD	BW	WAT	BAT	QUAD

FIGURE 4



Cbl-deficient



Wild Type

FIGURE 5

ADIPOCYTE SIZE MALES

	diameter (μm)		VOLUME (pl/cell)		Lipid content (ng/cell)	
	AVG	SEM	AVG	SEM	AVG	SEM
WT	84.91	1.57	240.28	4.45	219.86	4.07
KO	49.44	0.90	82.43	1.25	75.42	1.14
KO 500	56.82	1.23	72	1.56	65.88	1.43

ADIPOCYTE SIZE FEMALES

	diameter (μm)		VOLUME (pl/cell)		Lipid content (ng/cell)	
	AVG	SEM	AVG	SEM	AVG	SEM
WT	80.48	2.32	204.6	5.9	187.3	5.4
KO	55.21	1.77	66.05	2.12	60.92	1.96

FIGURE 6

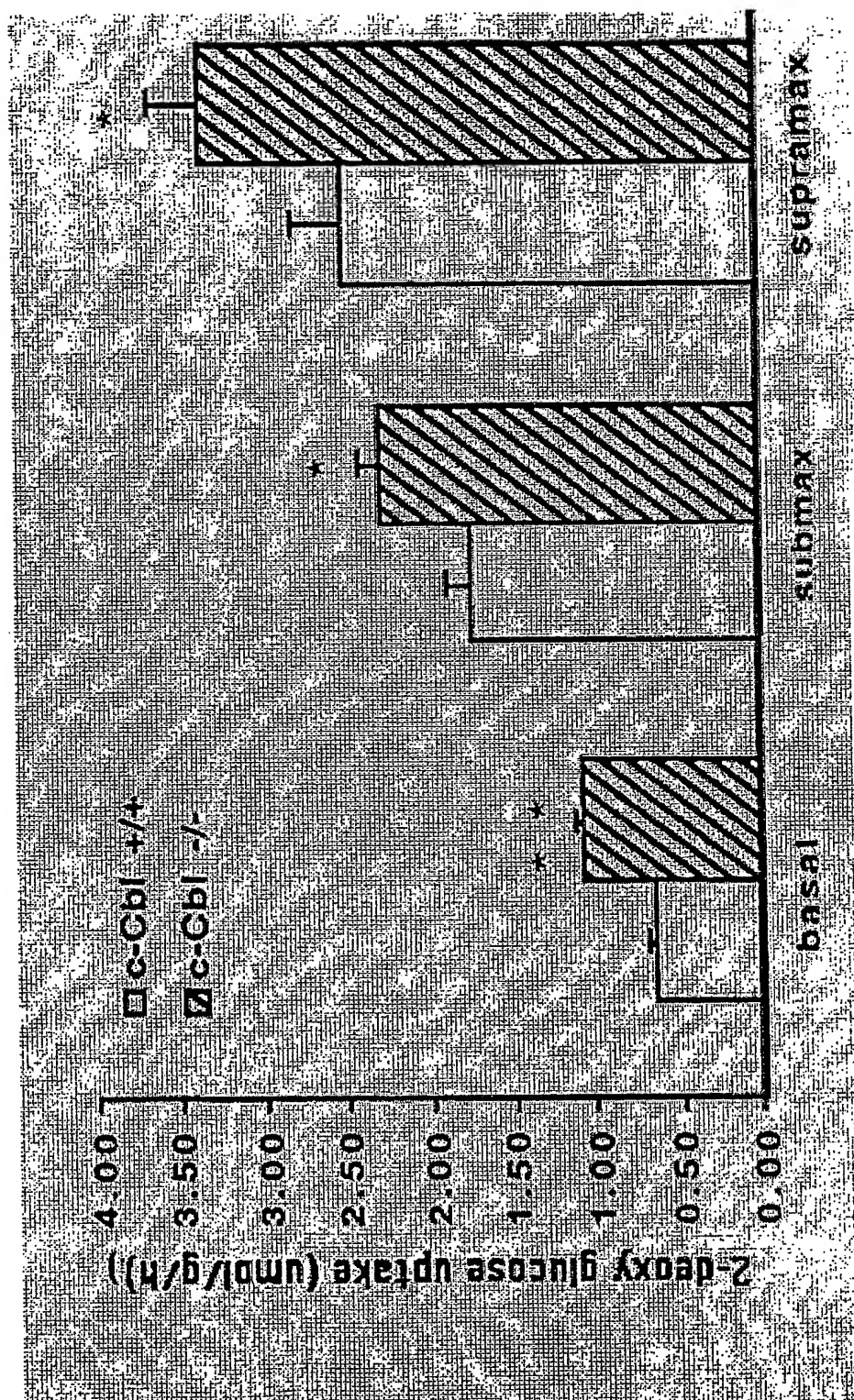


FIGURE 7A

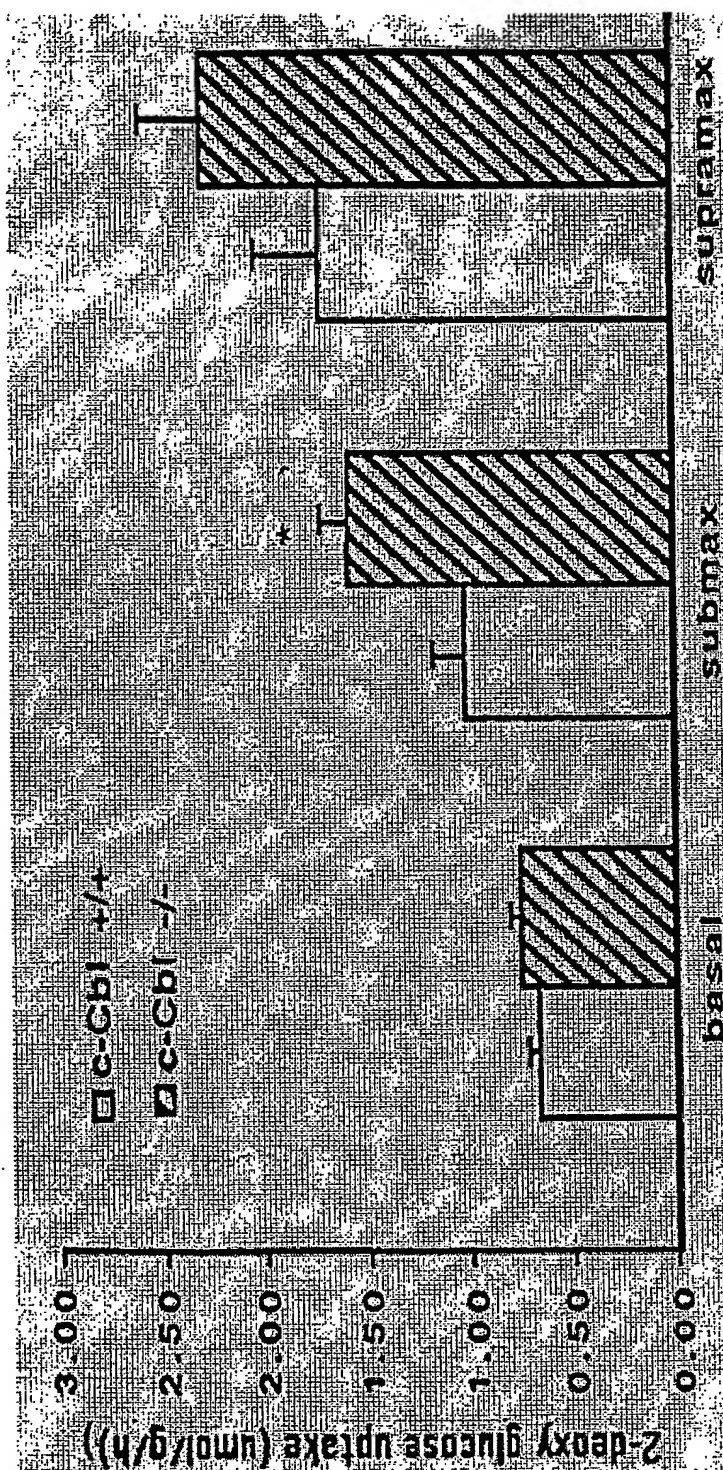


FIGURE 7B

9/9

10/539105

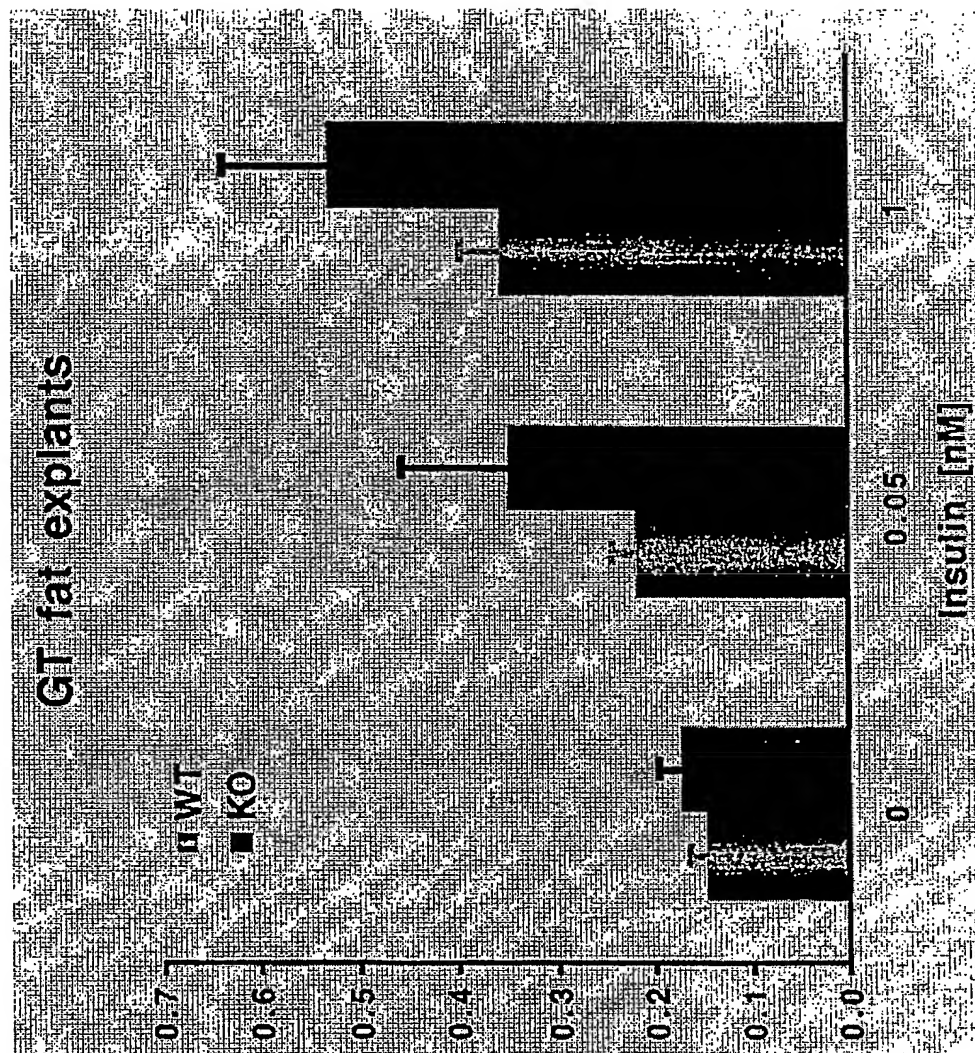


FIGURE 8

10/539105

JC17 Rec'd PCT/PTO 15 JUN 2003

SEQUENCE LISTING

<110> Garvan Institute of Medical Research

<120> Methods of treatment of feeding disorders or disorders of glucose uptake and for modifying metabolism and identifying therapeutic reagents therefor

<130> 502008/MRO

<150> AU 2002953393

<151> 2002-12-16

<150> AU 2003906285

<151> 2003-11-14

<160> 261

<170> PatentIn version 3.1

<210> 1

<211> 153

<212> PRT

<213> disrupted mouse Cbl

<400> 1

Met	Ala	Gly	Asn	Val	Lys	Lys	Ser	Ser	Gly	Ala	Gly	Gly	Gly	Gly	Ser
1				5					10					15	
Gly	Gly	Ser	Gly	Ala	Gly	Gly	Leu	Ile	Gly	Leu	Met	Lys	Asp	Ala	Phe
			20					25					30		
Gln	Pro	His	His	His	His	His	His	Leu	Ser	Pro	His	Pro	Pro	Cys	Thr
		35					40					45			
Val	Asp	Lys	Lys	Met	Val	Glu	Lys	Cys	Trp	Lys	Leu	Met	Asp	Lys	Val
	50					55					60				
Val	Arg	Leu	Cys	Gln	Asn	Pro	Asn	Val	Ala	Leu	Lys	Asn	Ser	Pro	Pro
65					70					75					80
Tyr	Ile	Leu	Asp	Leu	Leu	Pro	Asp	Thr	Tyr	Gln	His	Leu	Arg	Thr	Val
			85					90						95	
Leu	Ser	Arg	Tyr	Glu	Gly	Lys	Met	Glu	Thr	Leu	Gly	Glu	Asn	Glu	Tyr
			100					105					110		
Phe	Arg	Val	Phe	Met	Glu	Asn	Leu	Met	Lys	Lys	Thr	Lys	Gln	Thr	Ile
		115					120					125			
Ser	Leu	Phe	Lys	Glu	Gly	Lys	Glu	Arg	Met	Tyr	Glu	Glu	Asn	Ser	Gln
		130				135					140				
Pro	Arg	Arg	Asn	Leu	Thr	Lys	Leu	Ser							
145					150										

<210> 2

<211> 896

<212> PRT

<213> native full-length mouse Cbl

<400> 2

Met Ala Gly Asn Val Lys Lys Ser Ser Gly Ala Gly Gly Gly Gly Ser
1 5 10 15

Gly Gly Ser Gly Ala Gly Gly Leu Ile Gly Leu Met Lys Asp Ala Phe
20 25 30

Gln Pro His His His His His His Leu Ser Pro His Pro Pro Cys Thr
35 40 45

Val Asp Lys Lys Met Val Glu Lys Cys Trp Lys Leu Met Asp Lys Val
50 55 60

Val Arg Leu Cys Gln Asn Pro Asn Val Ala Leu Lys Asn Ser Pro Pro
65 70 75 80

Tyr Ile Leu Asp Leu Leu Pro Asp Thr Tyr Gln His Leu Arg Thr Val
85 90 95

Leu Ser Arg Tyr Glu Gly Lys Met Glu Thr Leu Gly Glu Asn Glu Tyr
100 105 110

Phe Arg Val Phe Met Glu Asn Leu Met Lys Lys Thr Lys Gln Thr Ile
115 120 125

Ser Leu Phe Lys Glu Gly Lys Glu Arg Met Tyr Glu Glu Asn Ser Gln
130 135 140

Pro Arg Arg Asn Leu Thr Lys Leu Ser Leu Ile Phe Ser His Met Leu
145 150 155 160

Ala Glu Leu Lys Gly Ile Phe Pro Ser Gly Leu Phe Gln Gly Asp Thr
165 170 175

Phe Arg Ile Thr Lys Ala Asp Ala Ala Glu Phe Trp Arg Lys Ala Phe
180 185 190

Gly Glu Lys Thr Ile Val Pro Trp Lys Ser Phe Arg Gln Ala Leu His
195 200 205

Glu Val His Pro Ile Ser Ser Gly Leu Glu Ala Met Ala Leu Lys Ser
210 215 220

Thr Ile Asp Leu Thr Cys Asn Asp Tyr Ile Ser Val Phe Glu Phe Asp
225 230 235 240

Ile Phe Thr Arg Leu Phe Gln Pro Trp Ser Ser Leu Leu Arg Asn Trp
245 250 255

Asn Ser Leu Ala Val Thr His Pro Gly Tyr Met Ala Phe Leu Thr Tyr
260 265 270

Asp Glu Val Lys Ala Arg Leu Gln Lys Phe Ile His Lys Pro Gly Ser
275 280 285

Tyr Ile Phe Arg Leu Ser Cys Thr Arg Leu Gly Gln Trp Ala Ile Gly
 290 295 300
 Tyr Val Thr Ala Asp Gly Asn Ile Leu Gln Thr Ile Pro His Asn Lys
 305 310 315 320
 Pro Leu Phe Gln Ala Leu Ile Asp Gly Phe Arg Glu Gly Phe Tyr Leu
 325 330 335
 Phe Pro Asp Gly Arg Asn Gln Asn Pro Asp Leu Thr Gly Leu Cys Glu
 340 345 350
 Pro Thr Pro Gln Asp His Ile Lys Val Thr Gln Ile Cys Ala Glu Asn
 355 360 365
 Asp Lys Asp Val Lys Ile Glu Pro Cys Gly His Leu Met Cys Thr Ser
 370 375 380
 Cys Leu Thr Ser Trp Gln Glu Ser Glu Gly Gln Gly Cys Pro Phe Cys
 385 390 395 400
 Arg Cys Glu Ile Lys Gly Thr Glu Pro Ile Val Val Asp Pro Phe Asp
 405 410 415
 Pro Arg Gly Ser Gly Ser Leu Leu Arg Gln Gly Ala Glu Gly Ala Pro
 420 425 430
 Ser Pro Asn Tyr Asp Asp Asp Asp Glu Arg Ala Asp Asp Ser Leu
 435 440 445
 Phe Met Met Lys Glu Leu Ala Gly Ala Lys Val Glu Arg Pro Ser Ser
 450 455 460
 Pro Phe Ser Met Ala Pro Gln Ala Ser Leu Pro Pro Val Pro Pro Arg
 465 470 475 480
 Leu Asp Leu Leu Gln Gln Arg Ala Pro Val Pro Ala Ser Thr Ser Val
 485 490 495
 Leu Gly Thr Ala Ser Lys Ala Ala Ser Gly Ser Leu His Lys Asp Lys
 500 505 510
 Pro Leu Pro Ile Pro Pro Thr Leu Arg Asp Leu Pro Pro Pro Pro Pro
 515 520 525
 Pro Asp Arg Pro Tyr Ser Val Gly Ala Glu Thr Arg Pro Gln Arg Arg
 530 535 540
 Pro Leu Pro Cys Thr Pro Gly Asp Cys Pro Ser Arg Asp Lys Leu Pro
 545 550 555 560
 Pro Val Pro Ser Ser Arg Pro Gly Asp Ser Trp Leu Ser Arg Thr Ile
 565 570 575
 Pro Lys Val Pro Val Ala Thr Pro Asn Pro Gly Asp Pro Trp Asn Gly
 580 585 590
 Arg Glu Leu Thr Asn Arg His Ser Leu Pro Phe Ser Leu Pro Ser Gln
 595 600 605

Met Glu Pro Arg Ala Asp Val Pro Arg Leu Gly Ser Thr Phe Ser Leu
610 615 620
Asp Thr Ser Met Thr Met Asn Ser Ser Pro Val Ala Gly Pro Glu Ser
625 630 635 640
Glu His Pro Lys Ile Lys Pro Ser Ser Ser Ala Asn Ala Ile Tyr Ser
645 650 655
Leu Ala Ala Arg Pro Leu Pro Met Pro Lys Leu Pro Pro Gly Glu Gln
660 665 670
Gly Glu Ser Glu Glu Asp Thr Glu Tyr Met Thr Pro Thr Ser Arg Pro
675 680 685
Val Gly Val Gln Lys Pro Glu Pro Lys Arg Pro Leu Glu Ala Thr Gln
690 695 700
Ser Ser Arg Ala Cys Asp Cys Asp Gln Gln Ile Asp Ser Cys Thr Tyr
705 710 715 720
Glu Ala Met Tyr Thr Ile Gln Ser Gln Ala Leu Ser Val Ala Glu Asn
725 730 735
Ser Ala Ser Gly Glu Gly Asn Leu Ala Thr Ala His Thr Ser Thr Gly
740 745 750
Pro Glu Glu Ser Glu Asn Glu Asp Asp Gly Tyr Asp Val Pro Lys Pro
755 760 765
Pro Val Pro Ala Val Leu Ala Arg Arg Thr Leu Ser Asp Ile Ser Asn
770 775 780
Ala Ser Ser Ser Phe Gly Trp Leu Ser Leu Asp Gly Asp Pro Thr Asn
785 790 795 800
Phe Asn Glu Gly Ser Gln Val Pro Glu Arg Pro Pro Lys Pro Phe Pro
805 810 815
Arg Arg Ile Asn Ser Glu Arg Lys Ala Ser Ser Tyr Gln Gln Gly Gly
820 825 830
Gly Ala Thr Ala Asn Pro Val Ala Thr Ala Pro Ser Pro Gln Leu Ser
835 840 845
Ser Glu Ile Glu Arg Leu Met Ser Gln Gly Tyr Ser Tyr Gln Asp Ile
850 855 860
Gln Lys Ala Leu Val Ile Ala His Asn Asn Ile Glu Met Ala Lys Asn
865 870 875 880
Ile Leu Arg Glu Phe Val Ser Ile Ser Ser Pro Ala His Val Ala Thr
885 890 895

<210> 3

<211> 906

<212> PRT

<213> native full-length human c-Cbl

<400> 3

Met Ala Gly Asn Val Lys Lys Ser Ser Gly Ala Gly Gly Gly Thr Gly
 1 5 10 15
 Ser Gly Gly Ser Gly Ser Gly Gly Leu Ile Gly Leu Met Lys Asp Ala
 20 25 30
 Phe Gln Pro His His His His His His His Leu Ser Pro His Pro Pro
 35 40 45
 Gly Thr Val Asp Lys Lys Met Val Glu Lys Cys Trp Lys Leu Met Asp
 50 55 60
 Lys Val Val Arg Leu Cys Gln Asn Pro Lys Leu Ala Leu Lys Asn Ser
 65 70 75 80
 Pro Pro Tyr Ile Leu Asp Leu Leu Pro Asp Thr Tyr Gln His Leu Arg
 85 90 95
 Thr Ile Leu Ser Arg Tyr Glu Gly Lys Met Glu Thr Leu Gly Glu Asn
 100 105 110
 Glu Tyr Phe Arg Val Phe Met Glu Asn Leu Met Lys Lys Thr Lys Gln
 115 120 125
 Thr Ile Ser Leu Phe Lys Glu Gly Lys Glu Arg Met Tyr Glu Glu Asn
 130 135 140
 Ser Gln Pro Arg Arg Asn Leu Thr Lys Leu Ser Leu Ile Phe Ser His
 145 150 155 160
 Met Leu Ala Glu Leu Lys Gly Ile Phe Pro Ser Gly Leu Phe Gln Gly
 165 170 175
 Asp Thr Phe Arg Ile Thr Lys Ala Asp Ala Ala Glu Phe Trp Arg Lys
 180 185 190
 Ala Phe Gly Glu Lys Thr Ile Val Pro Trp Lys Ser Phe Arg Gln Ala
 195 200 205
 Leu His Glu Val His Pro Ile Ser Ser Gly Leu Glu Ala Met Ala Leu
 210 215 220
 Lys Ser Thr Ile Asp Leu Thr Cys Asn Asp Tyr Ile Ser Val Phe Glu
 225 230 235 240
 Phe Asp Ile Phe Thr Arg Leu Phe Gln Pro Trp Ser Ser Leu Leu Arg
 245 250 255
 Asn Trp Asn Ser Leu Ala Val Thr His Pro Gly Tyr Met Ala Phe Leu
 260 265 270
 Thr Tyr Asp Glu Val Lys Ala Arg Leu Gln Lys Phe Ile His Lys Pro
 275 280 285
 Gly Ser Tyr Ile Phe Arg Leu Ser Cys Thr Arg Leu Gly Gln Trp Ala

290	295	300
Ile Gly Tyr Val Thr Ala Asp Gly Asn Ile Leu Gln Thr Ile Pro His 305 310 315 320		
Asn Lys Pro Leu Phe Gln Ala Leu Ile Asp Gly Phe Arg Glu Gly Phe 325 330 335		
Tyr Leu Phe Pro Asp Gly Arg Asn Gln Asn Pro Asp Leu Thr Gly Leu 340 345 350		
Cys Glu Pro Thr Pro Gln Asp His Ile Lys Val Thr Gln Glu Gln Tyr 355 360 365		
Glu Leu Tyr Cys Glu Met Gly Ser Thr Phe Gln Leu Cys Lys Ile Cys 370 375 380		
Ala Glu Asn Asp Lys Asp Val Lys Ile Glu Pro Cys Gly His Leu Met 385 390 395 400		
Cys Thr Ser Cys Leu Thr Ser Trp Gln Glu Ser Glu Gly Gln Gly Cys 405 410 415		
Pro Phe Cys Arg Cys Glu Ile Lys Gly Thr Glu Pro Ile Val Val Asp 420 425 430		
Pro Phe Asp Pro Arg Gly Ser Gly Ser Leu Leu Arg Gln Gly Ala Glu 435 440 445		
Gly Ala Pro Ser Pro Asn Tyr Asp Asp Asp Asp Asp Glu Arg Ala Asp 450 455 460		
Asp Thr Leu Phe Met Met Lys Glu Leu Ala Gly Ala Lys Val Glu Arg 465 470 475 480		
Pro Pro Ser Pro Phe Ser Met Ala Pro Gln Ala Ser Leu Pro Pro Val 485 490 495		
Pro Pro Arg Leu Asp Leu Leu Pro Gln Arg Val Cys Val Pro Ser Ser 500 505 510		
Ala Ser Ala Leu Gly Thr Ala Ser Lys Ala Ala Ser Gly Ser Leu His 515 520 525		
Lys Asp Lys Pro Leu Pro Val Pro Pro Thr Leu Arg Asp Leu Pro Pro 530 535 540		
Pro Pro Pro Pro Asp Arg Pro Tyr Ser Val Gly Ala Glu Ser Arg Pro 545 550 555 560		
Gln Arg Arg Pro Leu Pro Cys Thr Pro Gly Asp Cys Pro Ser Arg Asp 565 570 575		
Lys Leu Pro Pro Val Pro Ser Ser Arg Leu Gly Asp Ser Trp Leu Pro 580 585 590		
Arg Pro Ile Pro Lys Val Pro Val Ser Ala Pro Ser Ser Ser Asp Pro 595 600 605		
Trp Thr Gly Arg Glu Leu Thr Asn Arg His Ser Leu Pro Phe Ser Leu 610 615 620		

Pro Ser Gln Met Glu Pro Arg Pro Asp Val Pro Arg Leu Gly Ser Thr
 625 630 635 640
 Phe Ser Leu Asp Thr Ser Met Ser Met Asn Ser Ser Pro Leu Val Gly
 645 650 655
 Pro Glu Cys Asp His Pro Lys Ile Lys Pro Ser Ser Ser Ala Asn Ala
 660 665 670
 Ile Tyr Ser Leu Ala Ala Arg Pro Leu Pro Val Pro Lys Leu Pro Pro
 675 680 685
 Gly Glu Gln Cys Glu Gly Glu Glu Asp Thr Glu Tyr Met Thr Pro Ser
 690 695 700
 Ser Arg Pro Leu Arg Pro Leu Asp Thr Ser Gln Ser Ser Arg Ala Cys
 705 710 715 720
 Asp Cys Asp Gln Gln Ile Asp Ser Cys Thr Tyr Glu Ala Met Tyr Asn
 725 730 735
 Ile Gln Ser Gln Ala Pro Ser Ile Thr Glu Ser Ser Thr Phe Gly Glu
 740 745 750
 Gly Asn Leu Ala Ala Ala His Ala Asn Thr Gly Pro Glu Glu Ser Glu
 755 760 765
 Asn Glu Asp Asp Gly Tyr Asp Val Pro Lys Pro Pro Val Pro Ala Val
 770 775 780
 Leu Ala Arg Arg Thr Leu Ser Asp Ile Ser Asn Ala Ser Ser Ser Phe
 785 790 795 800
 Gly Trp Leu Ser Leu Asp Gly Asp Pro Thr Thr Asn Val Thr Glu Gly
 805 810 815
 Ser Gln Val Pro Glu Arg Pro Pro Lys Pro Phe Pro Arg Arg Ile Asn
 820 825 830
 Ser Glu Arg Lys Ala Gly Ser Cys Gln Gln Gly Ser Gly Pro Ala Ala
 835 840 845
 Ser Ala Ala Thr Ala Ser Pro Gln Leu Ser Ser Glu Ile Glu Asn Leu
 850 855 860
 Met Ser Gln Gly Tyr Ser Tyr Gln Asp Ile Gln Lys Ala Leu Val Ile
 865 870 875 880
 Ala Gln Asn Asn Ile Glu Met Ala Lys Asn Ile Leu Arg Glu Phe Val
 885 890 895
 Ser Ile Ser Ser Pro Ala His Val Ala Thr
 900 905

<210> 4

<211> 21

<212> DNA

<213> siRNA sense strand oligonucleotide

<400> 4

cgtgaagaag agctctgggt t 21

<210> 5
<211> 21
<212> DNA
<213> siRNA sense strand oligonucleotide

<400> 5
gaagatgggtg gagaagtgct t 21

<210> 6
<211> 21
<212> DNA
<213> siRNA sense strand oligonucleotide

<400> 6
gatgggtggag aagtgctggt t 21

<210> 7
<211> 21
<212> DNA
<213> siRNA sense strand oligonucleotide

<400> 7
gtgctggaag ctcattgact t 21

<210> 8
<211> 21
<212> DNA
<213> siRNA sense strand oligonucleotide

<400> 8
gctcatggac aaggtggtgt t 21

<210> 9
<211> 21
<212> DNA
<213> siRNA sense strand oligonucleotide

<400> 9
ggtggtgcgg ttgtgtcagt t 21

<210> 10
<211> 21
<212> DNA
<213> siRNA sense strand oligonucleotide

<400> 10
cccaaagctg gcgctaaagt t 21

<210> 11
<211> 21
<212> DNA
<213> siRNA sense strand oligonucleotide

<400> 11
cccaaagctg gcgctaaagt t 21

<210> 12
<211> 21
<212> DNA

9/88

<213> siRNA sense strand oligonucleotide

<400> 12
agctggcgct aaagaatagt t 21

<210> 13
<211> 21
<212> DNA
<213> siRNA sense strand oligonucleotide

<400> 13
agaatagccc accttatatt t 21

<210> 14
<211> 21
<212> DNA
<213> siRNA sense strand oligonucleotide

<400> 14
tagcccacct tatatcttat t 21

<210> 15
<211> 21
<212> DNA
<213> siRNA sense strand oligonucleotide

<400> 15
gatatgaggg gaagatggat t 21

<210> 16
<211> 21
<212> DNA
<213> siRNA sense strand oligonucleotide

<400> 16
gatggagaca cttggagaat t 21

<210> 17
<211> 21
<212> DNA
<213> siRNA sense strand oligonucleotide

<400> 17
ctaagcaaac cataagcctt t 21

<210> 18
<211> 21
<212> DNA
<213> siRNA sense strand oligonucleotide

<400> 18
gcaaaccata agcctcttct t 21

<210> 19
<211> 21
<212> DNA
<213> siRNA sense strand oligonucleotide

<400> 19
accataagcc tcttcaaggt t 21

<210> 20
<211> 21
<212> DNA
<213> siRNA sense strand oligonucleotide

<400> 20
gcctcttcaa ggagggaaat t 21

<210> 21
<211> 21
<212> DNA
<213> siRNA sense strand oligonucleotide

<400> 21
gaaagaatgt atgaggagat t 21

<210> 22
<211> 21
<212> DNA
<213> siRNA sense strand oligonucleotide

<400> 22
agaatgtatg aggagaattt t 21

<210> 23
<211> 21
<212> DNA
<213> siRNA sense strand oligonucleotide

<400> 23
tgtatgagga gaattctcat t 21

<210> 24
<211> 21
<212> DNA
<213> siRNA sense strand oligonucleotide

<400> 24
ttctcagcct aggcgaaact t 21

<210> 25
<211> 21
<212> DNA
<213> siRNA sense strand oligonucleotide

<400> 25
acctaacc aa actgtccctt t 21

<210> 26
<211> 21
<212> DNA
<213> siRNA sense strand oligonucleotide

<400> 26
ccaaactgtc cctcatcttt t 21

<210> 27
<211> 21
<212> DNA

11/88

<213> siRNA sense strand oligonucleotide

<400> 27
actgtccctc atcttcagct t 21

<210> 28
<211> 21
<212> DNA
<213> siRNA sense strand oligonucleotide

<400> 28
ggaatctttc caagtggaat t 21

<210> 29
<211> 21
<212> DNA
<213> siRNA sense strand oligonucleotide

<400> 29
tctttccaag tggactcttt t 21

<210> 30
<211> 21
<212> DNA
<213> siRNA sense strand oligonucleotide

<400> 30
gtggactctt tcaggagat t 21

<210> 31
<211> 21
<212> DNA
<213> siRNA sense strand oligonucleotide

<400> 31
agcagatgct gcggaatttt t 21

<210> 32
<211> 21
<212> DNA
<213> siRNA sense strand oligonucleotide

<400> 32
gacaatagtc ccttggaagt t 21

<210> 33
<211> 21
<212> DNA
<213> siRNA sense strand oligonucleotide

<400> 33
tagtccttg gaagagcttt t 21

<210> 34
<211> 21
<212> DNA
<213> siRNA sense strand oligonucleotide

<400> 34
gagctttcga caggctctat t 21

<210> 35
<211> 21
<212> DNA
<213> siRNA sense strand oligonucleotide

<400> 35
gtgcatccca tcagttctgt t 21

<210> 36
<211> 21
<212> DNA
<213> siRNA sense strand oligonucleotide

<400> 36
atccactatt gatctgacct t 21

<210> 37
<211> 21
<212> DNA
<213> siRNA sense strand oligonucleotide

<400> 37
tttgacatct ttacccgact t 21

<210> 38
<211> 21
<212> DNA
<213> siRNA sense strand oligonucleotide

<400> 38
ttggaacagc cttgctgtat t 21

<210> 39
<211> 21
<212> DNA
<213> siRNA sense strand oligonucleotide

<400> 39
cagccttgct gtaactcatt t 21

<210> 40
<211> 21
<212> DNA
<213> siRNA sense strand oligonucleotide

<400> 40
ctcatcctgg ctacatggct t 21

<210> 41
<211> 21
<212> DNA
<213> siRNA sense strand oligonucleotide

<400> 41
gtgaaagctc ggctccagat t 21

<210> 42
<211> 21
<212> DNA
<213> siRNA sense strand oligonucleotide

<400> 42
agctcggtc cagaaattct t 21

<210> 43
<211> 21
<212> DNA
<213> siRNA sense strand oligonucleotide

<400> 43
attcattcac aaacctggct t 21

<210> 44
<211> 21
<212> DNA
<213> siRNA sense strand oligonucleotide

<400> 44
acctggcagt tatatcttct t 21

<210> 45
<211> 21
<212> DNA
<213> siRNA sense strand oligonucleotide

<400> 45
cattctccag acaatccctt t 21

<210> 46
<211> 21
<212> DNA
<213> siRNA sense strand oligonucleotide

<400> 46
tccctcacaa taaacctctt t 21

<210> 47
<211> 21
<212> DNA
<213> siRNA sense strand oligonucleotide

<400> 47
taaacctctc ttccaagcat t 21

<210> 48
<211> 21
<212> DNA
<213> siRNA sense strand oligonucleotide

<400> 48
acctctcttc caagcactgt t 21

<210> 49
<211> 21
<212> DNA
<213> siRNA sense strand oligonucleotide

<400> 49
gcactgattg atggcttcat t 21

<210> 50
<211> 21

<212> DNA
<213> siRNA sense strand oligonucleotide

<400> 50
ggcttctatt tgtttcctgt t 21

<210> 51
<211> 21
<212> DNA
<213> siRNA sense strand oligonucleotide

<400> 51
atcagaatcc tgatctgact t 21

<210> 52
<211> 21
<212> DNA
<213> siRNA sense strand oligonucleotide

<400> 52
tcctgatctg actggcttat t 21

<210> 53
<211> 21
<212> DNA
<213> siRNA sense strand oligonucleotide

<400> 53
ccaactcccc aagaccatat t 21

<210> 54
<211> 21
<212> DNA
<213> siRNA sense strand oligonucleotide

<400> 54
ctccccaaga ccatatcaat t 21

<210> 55
<211> 21
<212> DNA
<213> siRNA sense strand oligonucleotide

<400> 55
gaccatatca aagtgaccct t 21

<210> 56
<211> 21
<212> DNA
<213> siRNA sense strand oligonucleotide

<400> 56
agtgaccag gaacaatatt t 21

<210> 57
<211> 21
<212> DNA
<213> siRNA sense strand oligonucleotide

<400> 57
caatatgaat tatactgtgt t 21

<210> 58
<211> 21
<212> DNA
<213> siRNA sense strand oligonucleotide

<400> 58
tatgaattat actgtgagat t 21

<210> 59
<211> 21
<212> DNA
<213> siRNA sense strand oligonucleotide

<400> 59
ttatactgtg agatgggctt t 21

<210> 60
<211> 21
<212> DNA
<213> siRNA sense strand oligonucleotide

<400> 60
tgataaggat gtaaagattt t 21

<210> 61
<211> 21
<212> DNA
<213> siRNA sense strand oligonucleotide

<400> 61
ggatgtaaag attgagccct t 21

<210> 62
<211> 21
<212> DNA
<213> siRNA sense strand oligonucleotide

<400> 62
agattgagcc ctgtggacat t 21

<210> 63
<211> 21
<212> DNA
<213> siRNA sense strand oligonucleotide

<400> 63
tcagaaggctc agggctgtct t 21

<210> 64
<211> 21
<212> DNA
<213> siRNA sense strand oligonucleotide

<400> 64
ggtcagggt gtcctttctt t 21

<210> 65
<211> 21
<212> DNA

<213> siRNA sense strand oligonucleotide

<400> 65

attaaaggta ctgaacccat t

21

<210> 66

<211> 21

<212> DNA

<213> siRNA sense strand oligonucleotide

<400> 66

aggtactgaa cccatcgtgt t

21

<210> 67

<211> 21

<212> DNA

<213> siRNA sense strand oligonucleotide

<400> 67

cccatcgtgg tagatccgtt t

21

<210> 68

<211> 21

<212> DNA

<213> siRNA sense strand oligonucleotide

<400> 68

attatgatga tgatgatgat t

21

<210> 69

<211> 21

<212> DNA

<213> siRNA sense strand oligonucleotide

<400> 69

cgagctgatg atactctctt t

21

<210> 70

<211> 21

<212> DNA

<213> siRNA sense strand oligonucleotide

<400> 70

ggaattggct ggtgccaagt t

21

<210> 71

<211> 21

<212> DNA

<213> siRNA sense strand oligonucleotide

<400> 71

ttggctgggtg ccaagggtgt t

21

<210> 72

<211> 21

<212> DNA

<213> siRNA sense strand oligonucleotide

<400> 72

cggccgcctt ctccattctt t

21

<210> 73
<211> 21
<212> DNA
<213> siRNA sense strand oligonucleotide

<400> 73
gtgcttctgc tcttggaact t 21

<210> 74
<211> 21
<212> DNA
<213> siRNA sense strand oligonucleotide

<400> 74
ctgcttctaa ggctgcttct t 21

<210> 75
<211> 21
<212> DNA
<213> siRNA sense strand oligonucleotide

<400> 75
ggctgcttct ggctcccttt t 21

<210> 76
<211> 21
<212> DNA
<213> siRNA sense strand oligonucleotide

<400> 76
agacaaacca ttgccagtat t 21

<210> 77
<211> 21
<212> DNA
<213> siRNA sense strand oligonucleotide

<400> 77
accattgccca gtacctccct t 21

<210> 78
<211> 21
<212> DNA
<213> siRNA sense strand oligonucleotide

<400> 78
tcccgcacctc aaagacgcct t 21

<210> 79
<211> 21
<212> DNA
<213> siRNA sense strand oligonucleotide

<400> 79
agacgcccct tgccttgat t 21

<210> 80
<211> 21
<212> DNA
<213> siRNA sense strand oligonucleotide

<400> 80
tccccaagt accagtatct t 21

<210> 81
<211> 21
<212> DNA
<213> siRNA sense strand oligonucleotide

<400> 81
agtaccagta tctgccccat t 21

<210> 82
<211> 21
<212> DNA
<213> siRNA sense strand oligonucleotide

<400> 82
gttcagtgga tccctggact t 21

<210> 83

<211> 21
<212> DNA
<213> siRNA sense strand oligonucleotide

<400> 83
gagaattaac caaccggcat t 21

<210> 84
<211> 21
<212> DNA
<213> siRNA sense strand oligonucleotide

<400> 84
ttaaccaacc ggcactcact t 21

<210> 85
<211> 21
<212> DNA
<213> siRNA sense strand oligonucleotide

<400> 85
ccaaccggca ctacttcct t 21

<210> 86
<211> 21
<212> DNA
<213> siRNA sense strand oligonucleotide

<400> 86
ccggcactca cttccatttt t 21

<210> 87
<211> 21
<212> DNA
<213> siRNA sense strand oligonucleotide

<400> 87
atggagccca gaccagatgt t 21

19/88

<210> 88
<211> 21
<212> DNA
<213> siRNA sense strand oligonucleotide

<400> 88
gcacgttcag tctggatact t 21

<210> 89
<211> 21
<212> DNA
<213> siRNA sense strand oligonucleotide

<400> 89
tagcagccca ttagtaggtt t 21

<210> 90
<211> 21
<212> DNA
<213> siRNA sense strand oligonucleotide

<400> 90
tcaaaccttc ctcactctgt t 21

<210> 91
<211> 21
<212> DNA
<213> siRNA sense strand oligonucleotide

<400> 91
accttcctca tctgccatt t 21

<210> 92
<211> 21
<212> DNA
<213> siRNA sense strand oligonucleotide

<400> 92
tgccatttat tctctggctt t 21

<210> 93
<211> 21
<212> DNA
<213> siRNA sense strand oligonucleotide

<400> 93
ctgccacctg gggagcaatt t 21

<210> 94
<211> 21
<212> DNA
<213> siRNA sense strand oligonucleotide

<400> 94
tgtgagggtg aaggagacat t 21

<210> 95
<211> 21
<212> DNA

20/88

<213> siRNA sense strand oligonucleotide

<400> 95
gaggacacag agtacatgat t 21

<210> 96
<211> 21
<212> DNA
<213> siRNA sense strand oligonucleotide

<400> 96
gcaatgtata atattcagtt t 21

<210> 97
<211> 21
<212> DNA
<213> siRNA sense strand oligonucleotide

<400> 97
tgtataatat tcagtcccat t 21

<210> 98
<211> 21
<212> DNA
<213> siRNA sense strand oligonucleotide

<400> 98
tattcagttcc caggcgccat t 21

<210> 99
<211> 21
<212> DNA
<213> siRNA sense strand oligonucleotide

<400> 99
cactgggtccc gaggagtcac t 21

<210> 100
<211> 21
<212> DNA
<213> siRNA sense strand oligonucleotide

<400> 100
tgaggatgat gggatatgatt t 21

<210> 101
<211> 21
<212> DNA
<213> siRNA sense strand oligonucleotide

<400> 101
ctctctcaga tatctctaatt t 21

<210> 102
<211> 21
<212> DNA
<213> siRNA sense strand oligonucleotide

<400> 102
tgccagctcc tcctttggct t 21

<210> 103
<211> 21
<212> DNA
<213> siRNA sense strand oligonucleotide

<400> 103
caaatgtcac tgaaggttct t 21

<210> 104
<211> 21
<212> DNA
<213> siRNA sense strand oligonucleotide

<400> 104
atgtcactga aggttcccat t 21

<210> 105
<211> 21
<212> DNA
<213> siRNA sense strand oligonucleotide

<400> 105
ggttccaag ttcccgagat t 21

<210> 106
<211> 21
<212> DNA
<213> siRNA sense strand oligonucleotide

<400> 106
gttcccgaga ggcctccaat t 21

<210> 107
<211> 21
<212> DNA
<213> siRNA sense strand oligonucleotide

<400> 107
ccattccgc ggagaatcat t 21

<210> 108
<211> 21
<212> DNA
<213> siRNA sense strand oligonucleotide

<400> 108
tcaactctga acggaaagct t 21

<210> 109
<211> 21
<212> DNA
<213> siRNA sense strand oligonucleotide

<400> 109
ctctgaacgg aaagctggct t 21

<210> 110
<211> 21
<212> DNA
<213> siRNA sense strand oligonucleotide

<400> 110
cggaagctg gcagctgtct t 21

<210> 111
<211> 21
<212> DNA
<213> siRNA sense strand oligonucleotide

<400> 111
agctggcagc tgtcagcaat t 21

<210> 112
<211> 21
<212> DNA
<213> siRNA sense strand oligonucleotide

<400> 112
cctcatgagt caggggtact t 21

<210> 113
<211> 21
<212> DNA
<213> siRNA sense strand oligonucleotide

<400> 113
agctttggtc attgcccagt t 21

<210> 114
<211> 21
<212> DNA
<213> siRNA sense strand oligonucleotide

<400> 114
caacatcgag atggccaaat t 21

<210> 115
<211> 21
<212> DNA
<213> siRNA sense strand oligonucleotide

<400> 115
acatcctccg ggaatttggt t 21

<210> 116
<211> 21
<212> DNA
<213> siRNA sense strand oligonucleotide

<400> 116
tttgttcca tttcttctct t 21

<210> 117
<211> 21
<212> DNA
<213> siRNA sense strand oligonucleotide

<400> 117
gtggcaccta gaagggcagt t 21

<210> 118
<211> 21
<212> DNA

<213> siRNA sense strand oligonucleotide

<400> 118
gggcaggagt tcctttggtt t 21

<210> 119
<211> 21
<212> DNA
<213> siRNA sense strand oligonucleotide

<400> 119
gtcttggcct ctctgtgggt t 21

<210> 120
<211> 21
<212> DNA
<213> siRNA sense strand oligonucleotide

<400> 120
gatttcaaag tggtagaatt t 21

<210> 121
<211> 21
<212> DNA
<213> siRNA sense strand oligonucleotide

<400> 121
tggagcagct agtatgtttt t 21

<210> 122
<211> 21
<212> DNA
<213> siRNA antisense strand oligonucleotide

<400> 122
cccagagctc ttcttcacgt t 21

<210> 123
<211> 21
<212> DNA
<213> siRNA antisense strand oligonucleotide

<400> 123
gcacttctcc accatcttct t 21

<210> 124
<211> 21
<212> DNA
<213> siRNA antisense strand oligonucleotide

<400> 124
ccagcacttc tccacatct t 21

<210> 125
<211> 21
<212> DNA
<213> siRNA antisense strand oligonucleotide

<400> 125
gtccatgagc ttccagcact t 21

<210> 126
<211> 21
<212> DNA
<213> siRNA antisense strand oligonucleotide

<400> 126
caccaccttg tccatgagct t 21

<210> 127
<211> 21
<212> DNA
<213> siRNA antisense strand oligonucleotide

<400> 127
ctgacacaac cgcaccacct t 21

<210> 128
<211> 21
<212> DNA
<213> siRNA antisense strand oligonucleotide

<400> 128
cttttagcgcc agctttgggt t 21

<210> 129
<211> 21
<212> DNA
<213> siRNA antisense strand oligonucleotide

<400> 129
cttttagcgcc agctttgggt t 21

<210> 130
<211> 21
<212> DNA
<213> siRNA antisense strand oligonucleotide

<400> 130
ctattcttta gcgccagctt t 21

<210> 131
<211> 21
<212> DNA
<213> siRNA antisense strand oligonucleotide

<400> 131
atataaggtg ggctattctt t 21

<210> 132
<211> 21
<212> DNA
<213> siRNA antisense strand oligonucleotide

<400> 132
taagatataa ggtgggctat t 21

<210> 133
<211> 21
<212> DNA
<213> siRNA antisense strand oligonucleotide

<400> 133
tccatcttcc cctcatatct t 21

<210> 134
<211> 21
<212> DNA
<213> siRNA antisense strand oligonucleotide

<400> 134
ttctccaagt gtctccatct t 21

<210> 135
<211> 21
<212> DNA
<213> siRNA antisense strand oligonucleotide

<400> 135
aggcttatgg tttgcttagt t 21

<210> 136
<211> 21
<212> DNA
<213> siRNA antisense strand oligonucleotide

<400> 136
gaagaggctt atggtttgct t 21

<210> 137
<211> 21
<212> DNA
<213> siRNA antisense strand oligonucleotide

<400> 137
ccttgaagag gcttatggtt t 21

<210> 138
<211> 21
<212> DNA
<213> siRNA antisense strand oligonucleotide

<400> 138
tttcctcct tgaagaggct t 21

<210> 139
<211> 21
<212> DNA
<213> siRNA antisense strand oligonucleotide

<400> 139
tctcctcata cattctttct t 21

<210> 140
<211> 21
<212> DNA
<213> siRNA antisense strand oligonucleotide

<400> 140
aattctcctc atacattctt t 21

<210> 141
<211> 21

<212> DNA
<213> siRNA antisense strand oligonucleotide

<400> 141
tgagaattct cctcatacat t 21

<210> 142
<211> 21
<212> DNA
<213> siRNA antisense strand oligonucleotide

<400> 142
gtttcgcta ggctgagaat t 21

<210> 143
<211> 21
<212> DNA
<213> siRNA antisense strand oligonucleotide

<400> 143
agggacagtt tggtaggtt t 21

<210> 144
<211> 21
<212> DNA
<213> siRNA antisense strand oligonucleotide

<400> 144
aagatgaggg acagtttggt t 21

<210> 145
<211> 21
<212> DNA
<213> siRNA antisense strand oligonucleotide

<400> 145
gctgaagatg agggacagtt t 21

<210> 146
<211> 21
<212> DNA
<213> siRNA antisense strand oligonucleotide

<400> 146
gtccacttgg aaagattcct t 21

<210> 147
<211> 21
<212> DNA
<213> siRNA antisense strand oligonucleotide

<400> 147
aagagtccac ttggaaagat t 21

<210> 148
<211> 21
<212> DNA
<213> siRNA antisense strand oligonucleotide

<400> 148
tctccctgaa agagtccact t 21

<210> 149
<211> 21
<212> DNA
<213> siRNA antisense strand oligonucleotide

<400> 149
aaattccgca gcatctgctt t 21

<210> 150
<211> 21
<212> DNA
<213> siRNA antisense strand oligonucleotide

<400> 150
cttccaaggg actattgtct t 21

<210> 151
<211> 21
<212> DNA
<213> siRNA antisense strand oligonucleotide

<400> 151
aagctcttcc aagggactat t 21

<210> 152
<211> 21
<212> DNA
<213> siRNA antisense strand oligonucleotide

<400> 152
tagagcctgt cgaaagctct t 21

<210> 153
<211> 21
<212> DNA
<213> siRNA antisense strand oligonucleotide

<400> 153
cagaactgat gggatgcact t 21

<210> 154
<211> 21
<212> DNA
<213> siRNA antisense strand oligonucleotide

<400> 154
ggtcagatca atagtggatt t 21

<210> 155
<211> 21
<212> DNA
<213> siRNA antisense strand oligonucleotide

<400> 155
gtcgggtaaa gatgtcaa t 21

<210> 156
<211> 21
<212> DNA

<213> siRNA antisense strand oligonucleotide

<400> 156

tacagcaagg ctgttccaat t

21

<210> 157

<211> 21

<212> DNA

<213> siRNA antisense strand oligonucleotide

<400> 157

atgagttaca gcaaggctgt t

21

<210> 158

<211> 21

<212> DNA

<213> siRNA antisense strand oligonucleotide

<400> 158

gccatgtagc caggatgagt t

21

<210> 159

<211> 21

<212> DNA

<213> siRNA antisense strand oligonucleotide

<400> 159

tetggagccg agctttcact t

21

<210> 160

<211> 21

<212> DNA

<213> siRNA antisense strand oligonucleotide

<400> 160

gaatttctgg agccgagctt t

21

<210> 161

<211> 21

<212> DNA

<213> siRNA antisense strand oligonucleotide

<400> 161

gccaggtttg tgaatgaatt t

21

<210> 162

<211> 21

<212> DNA

<213> siRNA antisense strand oligonucleotide

<400> 162

gaagatataa ctgccaggtt t

21

<210> 163

<211> 21

<212> DNA

<213> siRNA antisense strand oligonucleotide

<400> 163

agggattgtc tggagaatgt t

21

<210> 164
<211> 21
<212> DNA
<213> siRNA antisense strand oligonucleotide

<400> 164
agaggtttat tgtgaggat t 21

<210> 165
<211> 21
<212> DNA
<213> siRNA antisense strand oligonucleotide

<400> 165
tgcttggaag agaggtttat t 21

<210> 166
<211> 21
<212> DNA
<213> siRNA antisense strand oligonucleotide

<400> 166
cagtgccttg aagagaggtt t 21

<210> 167
<211> 21
<212> DNA
<213> siRNA antisense strand oligonucleotide

<400> 167
tgaagccatc aatcagtgct t 21

<210> 168
<211> 21
<212> DNA
<213> siRNA antisense strand oligonucleotide

<400> 168
caggaaacaa atagaagcct t 21

<210> 169
<211> 21
<212> DNA
<213> siRNA antisense strand oligonucleotide

<400> 169
gtcagatcag gattctgatt t 21

<210> 170
<211> 21
<212> DNA
<213> siRNA antisense strand oligonucleotide

<400> 170
taagccagtc agatcaggat t 21

<210> 171
<211> 21
<212> DNA

<213> siRNA antisense strand oligonucleotide

<400> 171
tatggtccttg gggagttggt t 21

<210> 172
<211> 21
<212> DNA
<213> siRNA antisense strand oligonucleotide

<400> 172
ttgatatggt cttggggagt t 21

<210> 173
<211> 21
<212> DNA
<213> siRNA antisense strand oligonucleotide

<400> 173
gggtcacttt gatatggtct t 21

<210> 174
<211> 21
<212> DNA
<213> siRNA antisense strand oligonucleotide

<400> 174
atattgttcc tgggtcactt t 21

<210> 175
<211> 21
<212> DNA
<213> siRNA antisense strand oligonucleotide

<400> 175
cacagtataa ttcatattgt t 21

<210> 176
<211> 21
<212> DNA
<213> siRNA antisense strand oligonucleotide

<400> 176
tctcacagta taattcatat t 21

<210> 177
<211> 21
<212> DNA
<213> siRNA antisense strand oligonucleotide

<400> 177
agcccatctc acagtataat t 21

<210> 178
<211> 21
<212> DNA
<213> siRNA antisense strand oligonucleotide

<400> 178
aatctttaca tccttatcat t 21

<210> 179
<211> 21
<212> DNA
<213> siRNA antisense strand oligonucleotide

<400> 179
gggctcaatc ttacatcct t 21

<210> 180
<211> 21
<212> DNA
<213> siRNA antisense strand oligonucleotide

<400> 180
tgtccacagg gctcaatctt t 21

<210> 181
<211> 21
<212> DNA
<213> siRNA antisense strand oligonucleotide

<400> 181
gacagccctg accttctgat t 21

<210> 182
<211> 21
<212> DNA
<213> siRNA antisense strand oligonucleotide

<400> 182
agaaaggaca gccctgacct t 21

<210> 183
<211> 21
<212> DNA
<213> siRNA antisense strand oligonucleotide

<400> 183
tgggttcagt acctttaatt t 21

<210> 184
<211> 21
<212> DNA
<213> siRNA antisense strand oligonucleotide

<400> 184
cacgatgggt tcagtacctt t 21

<210> 185
<211> 21
<212> DNA
<213> siRNA antisense strand oligonucleotide

<400> 185
acggatctac cacgatgggt t 21

<210> 186
<211> 21
<212> DNA
<213> siRNA antisense strand oligonucleotide

<400> 186
tcatcatcat catcataatt t 21

<210> 187
<211> 21
<212> DNA
<213> siRNA antisense strand oligonucleotide

<400> 187
agagagtatc atcagctcgt t 21

<210> 188
<211> 21
<212> DNA
<213> siRNA antisense strand oligonucleotide

<400> 188
cttggcacca gccaatcct t 21

<210> 189
<211> 21
<212> DNA
<213> siRNA antisense strand oligonucleotide

<400> 189
ccaccttggc accagccaat t 21

<210> 190
<211> 21
<212> DNA
<213> siRNA antisense strand oligonucleotide

<400> 190
agaatggaga aggcggccgt t 21

<210> 191
<211> 21
<212> DNA
<213> siRNA antisense strand oligonucleotide

<400> 191
gttccaagag cagaagcact t 21

<210> 192
<211> 21
<212> DNA
<213> siRNA antisense strand oligonucleotide

<400> 192
gaagcagcct tagaagcagt t 21

<210> 193
<211> 21
<212> DNA
<213> siRNA antisense strand oligonucleotide

<400> 193
aaggagacca gaagcagcct t 21

<210> 194
<211> 21

<212> DNA
<213> siRNA antisense strand oligonucleotide

<400> 194
tactggcaat ggtttgtctt t 21

<210> 195
<211> 21
<212> DNA
<213> siRNA antisense strand oligonucleotide

<400> 195
gggaggtact ggcaatggtt t 21

<210> 196
<211> 21
<212> DNA
<213> siRNA antisense strand oligonucleotide

<400> 196
ggcgtctttg aggtcgggat t 21

<210> 197
<211> 21
<212> DNA
<213> siRNA antisense strand oligonucleotide

<400> 197
tacaaggcaa ggggcgtctt t 21

<210> 198
<211> 21
<212> DNA
<213> siRNA antisense strand oligonucleotide

<400> 198
gatactggta ctttggggat t 21

<210> 199
<211> 21
<212> DNA
<213> siRNA antisense strand oligonucleotide

<400> 199
tggggcagat actggtactt t 21

<210> 200
<211> 21
<212> DNA
<213> siRNA antisense strand oligonucleotide

<400> 200
gtccagggat cactggaact t 21

<210> 201
<211> 21
<212> DNA
<213> siRNA antisense strand oligonucleotide

<400> 201
tgccggttg ttaattctct t 21

<210> 202
<211> 21
<212> DNA
<213> siRNA antisense strand oligonucleotide

<400> 202
gtgagtgccg gttggttaat t 21

<210> 203
<211> 21
<212> DNA
<213> siRNA antisense strand oligonucleotide

<400> 203
ggaagtgagt gccggttggt t 21

<210> 204
<211> 21
<212> DNA
<213> siRNA antisense strand oligonucleotide

<400> 204
aatggaagt gaggccggt t 21

<210> 205
<211> 21
<212> DNA
<213> siRNA antisense strand oligonucleotide

<400> 205
catctgtct gggctccatt t 21

<210> 206
<211> 21
<212> DNA
<213> siRNA antisense strand oligonucleotide

<400> 206
gtatccagac tgaacgtgct t 21

<210> 207
<211> 21
<212> DNA
<213> siRNA antisense strand oligonucleotide

<400> 207
acctactaat gggctgctat t 21

<210> 208
<211> 21
<212> DNA
<213> siRNA antisense strand oligonucleotide

<400> 208
gcagatgagg aaggtttgat t 21

<210> 209
<211> 21
<212> DNA

<213> siRNA antisense strand oligonucleotide

<400> 209

attggcagat gaggaaggtt t

21

<210> 210

<211> 21

<212> DNA

<213> siRNA antisense strand oligonucleotide

<400> 210

agccagagaa taaatggcat t

21

<210> 211

<211> 21

<212> DNA

<213> siRNA antisense strand oligonucleotide

<400> 211

attgctcccc aggtggcagt t

21

<210> 212

<211> 21

<212> DNA

<213> siRNA antisense strand oligonucleotide

<400> 212

tgtcctcttc accctcacat t

21

<210> 213

<211> 21

<212> DNA

<213> siRNA antisense strand oligonucleotide

<400> 213

tcatgtactc tgtgtcctct t

21

<210> 214

<211> 21

<212> DNA

<213> siRNA antisense strand oligonucleotide

<400> 214

actgaatatt atacattgct t

21

<210> 215

<211> 21

<212> DNA

<213> siRNA antisense strand oligonucleotide

<400> 215

tgggactgaa tattatacat t

21

<210> 216

<211> 21

<212> DNA

<213> siRNA antisense strand oligonucleotide

<400> 216

tggcgcctgg gactgaatat t

21

<210> 217
<211> 21
<212> DNA
<213> siRNA antisense strand oligonucleotide

<400> 217
tgactcctcg ggaccagtgt t 21

<210> 218
<211> 21
<212> DNA
<213> siRNA antisense strand oligonucleotide

<400> 218
atcatacca tcatcctcat t 21

<210> 219
<211> 21
<212> DNA
<213> siRNA antisense strand oligonucleotide

<400> 219
ttagagatat ctgagagagt t 21

<210> 220
<211> 21
<212> DNA
<213> siRNA antisense strand oligonucleotide

<400> 220
gccaaaggag gagctggcat t 21

<210> 221
<211> 21
<212> DNA
<213> siRNA antisense strand oligonucleotide

<400> 221
gaaccttcag tgacatttgt t 21

<210> 222
<211> 21
<212> DNA
<213> siRNA antisense strand oligonucleotide

<400> 222
tgggaacctt cagtgcatt t 21

<210> 223
<211> 21
<212> DNA
<213> siRNA antisense strand oligonucleotide

<400> 223
tctcgggaac ttgggaacct t 21

<210> 224
<211> 21
<212> DNA

<213> siRNA antisense strand oligonucleotide

<400> 224
ttggaggcct ctcggaact t 21

<210> 225
<211> 21
<212> DNA
<213> siRNA antisense strand oligonucleotide

<400> 225
tgattctccg cggaatggt t 21

<210> 226
<211> 21
<212> DNA
<213> siRNA antisense strand oligonucleotide

<400> 226
gctttccgtt cagagttgat t 21

<210> 227
<211> 21
<212> DNA
<213> siRNA antisense strand oligonucleotide

<400> 227
gccagctttc cgttcagagt t 21

<210> 228
<211> 21
<212> DNA
<213> siRNA antisense strand oligonucleotide

<400> 228
gacagctgcc agctttccgt t 21

<210> 229
<211> 21
<212> DNA
<213> siRNA antisense strand oligonucleotide

<400> 229
ttgctgacag ctgccagctt t 21

<210> 230
<211> 21
<212> DNA
<213> siRNA antisense strand oligonucleotide

<400> 230
gtacccctga ctcagaggt t 21

<210> 231
<211> 21
<212> DNA
<213> siRNA antisense strand oligonucleotide

<400> 231
ctgggcaatg accaaagctt t 21

<210> 232
<211> 21
<212> DNA
<213> siRNA antisense strand oligonucleotide

<400> 232
tttggccatc tcgatgttgt t 21

<210> 233
<211> 21
<212> DNA
<213> siRNA antisense strand oligonucleotide

<400> 233
acaaattccc ggaggatgtt t 21

<210> 234
<211> 21
<212> DNA
<213> siRNA antisense strand oligonucleotide

<400> 234
gagaagaaat ggaacaaat t 21

<210> 235
<211> 21
<212> DNA
<213> siRNA antisense strand oligonucleotide

<400> 235
ctgcccttct aggtgccact t 21

<210> 236
<211> 21
<212> DNA
<213> siRNA antisense strand oligonucleotide

<400> 236
accaaaggaa ctctgccct t 21

<210> 237
<211> 21
<212> DNA
<213> siRNA antisense strand oligonucleotide

<400> 237
cccacagaga gggcaagact t 21

<210> 238
<211> 21
<212> DNA
<213> siRNA antisense strand oligonucleotide

<400> 238
attcaccac tttgaaatct t 21

<210> 239
<211> 21
<212> DNA
<213> siRNA antisense strand oligonucleotide

<400> 239		
aaacatacta gctgctccat t		21
<210> 240		
<211> 3		
<212> DNA		
<213> shRNA loop sequence		
<400> 240		
ccc		3
<210> 241		
<211> 4		
<212> DNA		
<213> shRNA loop sequence		
<400> 241		
ttcg		4
<210> 242		
<211> 5		
<212> DNA		
<213> shRNA loop sequence		
<400> 242		
ccacc		5
<210> 243		
<211> 6		
<212> DNA		
<213> shRNA loop sequence		
<400> 243		
ctcgag		6
<210> 244		
<211> 6		
<212> DNA		
<213> shRNA loop sequence		
<400> 244		
aagctt		6
<210> 245		
<211> 7		
<212> DNA		
<213> shRNA loop sequence		
<400> 245		
ccacacc		7
<210> 246		
<211> 9		
<212> DNA		
<213> shRNA loop sequence		
<400> 246		
ttcaagaga		9
<210> 247		
<211> 2721		

<212> DNA

<213> c-Cbl G306E

<220>

<221> CDS

<222> (1)..(2718)

<223>

<400> 247

atg gcc ggc aac gtg aag aag agc tct ggg gcc ggg ggc ggc acg ggc	48
Met Ala Gly Asn Val Lys Lys Ser Ser Gly Ala Gly Gly Gly Thr Gly	
1 5 10 15	
tcc ggg ggc tcg ggt tcg ggt ggc ctg att ggg ctc atg aag gac gcc	96
Ser Gly Gly Ser Gly Ser Gly Gly Leu Ile Gly Leu Met Lys Asp Ala	
20 25 30	
ttc cag ccg cac cac cac cac cac cac ctc agc ccc cac ccg ccg	144
Phe Gln Pro His His His His His His His Leu Ser Pro His Pro Pro	
35 40 45	
ggg acg gtg gac aag aag atg gtg gag aag tgc tgg aag ctc atg gac	192
Gly Thr Val Asp Lys Lys Met Val Glu Lys Cys Trp Lys Leu Met Asp	
50 55 60	
aag gtg gtg cgg ttg tgt cag aac cca aag ctg gcg cta aag aat agc	240
Lys Val Val Arg Leu Cys Gln Asn Pro Lys Leu Ala Leu Lys Asn Ser	
65 70 75 80	
cca cct tat atc tta gac ctg cta cca gat acc tac cag cat ctc cgt	288
Pro Pro Tyr Ile Leu Asp Leu Leu Pro Asp Thr Tyr Gln His Leu Arg	
85 90 95	
act atc ttg tca aga tat gag ggg aag atg gag aca ctt gga gaa aat	336
Thr Ile Leu Ser Arg Tyr Glu Gly Lys Met Glu Thr Leu Gly Glu Asn	
100 105 110	
gag tat ttt agg gtg ttt atg gag aat ttg atg aag aaa act aag caa	384
Glu Tyr Phe Arg Val Phe Met Glu Asn Leu Met Lys Lys Thr Lys Gln	
115 120 125	
acc ata agc ctc ttc aag gag gga aaa gaa aga atg tat gag gag aat	432
Thr Ile Ser Leu Phe Lys Glu Gly Lys Glu Arg Met Tyr Glu Glu Asn	
130 135 140	
tct cag cct agg cga aac cta acc aaa ctg tcc ctc atc ttc agc cac	480
Ser Gln Pro Arg Arg Asn Leu Thr Lys Leu Ser Leu Ile Phe Ser His	
145 150 155 160	
atg ctg gca gaa cta aaa gga atc ttt cca agt gga ctc ttt cag gga	528
Met Leu Ala Glu Leu Lys Gly Ile Phe Pro Ser Gly Leu Phe Gln Gly	
165 170 175	
gac aca ttt cgg att act aaa gca gat gct gcg gaa ttt tgg aga aaa	576
Asp Thr Phe Arg Ile Thr Lys Ala Asp Ala Ala Glu Phe Trp Arg Lys	
180 185 190	
gct ttt ggg gaa aag aca ata gtc cct tgg aag agc ttt cga cag gct	624
Ala Phe Gly Glu Lys Thr Ile Val Pro Trp Lys Ser Phe Arg Gln Ala	
195 200 205	

cta cat gaa gtg cat ccc atc agt tct ggg ctg gag gcc atg gct ctg Leu His Glu Val His Pro Ile Ser Ser Gly Leu Glu Ala Met Ala Leu 210 215 220	672
aaa tcc act att gat ctg acc tgc aat gat tat att tcg gtt ttt gaa Lys Ser Thr Ile Asp Leu Thr Cys Asn Asp Tyr Ile Ser Val Phe Glu 225 230 235 240	720
ttt gac atc ttt acc cga ctc ttt cag ccc tgg tcc tct ttg ctc agg Phe Asp Ile Phe Thr Arg Leu Phe Gln Pro Trp Ser Ser Leu Leu Arg 245 250 255	768
aat tgg aac agc ctt gct gta act cat cct ggc tac atg gct ttt ttg Asn Trp Asn Ser Leu Ala Val Thr His Pro Gly Tyr Met Ala Phe Leu 260 265 270	816
acg tat gac gaa gtg aaa gct cgg ctc cag aaa ttc att cac aaa cct Thr Tyr Asp Glu Val Lys Ala Arg Leu Gln Lys Phe Ile His Lys Pro 275 280 285	864
ggc agt tat atc ttc cgg ctg agc tgt act cgt ctg ggt cag tgg gct Gly Ser Tyr Ile Phe Arg Leu Ser Cys Thr Arg Leu Gly Gln Trp Ala 290 295 300	912
att gag tat gtt act gct gat ggg aac att ctc cag aca atc cct cac Ile Glu Tyr Val Thr Ala Asp Gly Asn Ile Leu Gln Thr Ile Pro His 305 310 315 320	960
aat aaa cct ctc ttc caa gca ctg att gat ggc ttc agg gaa ggc ttc Asn Lys Pro Leu Phe Gln Ala Leu Ile Asp Gly Phe Arg Glu Gly Phe 325 330 335	1008
tat ttg ttt cct gat gga cga aat cag aat cct gat ctg act ggc tta Tyr Leu Phe Pro Asp Gly Arg Asn Gln Asn Pro Asp Leu Thr Gly Leu 340 345 350	1056
tgt gaa cca act ccc caa gac cat atc aaa gtg acc cag gaa caa tat Cys Glu Pro Thr Pro Gln Asp His Ile Lys Val Thr Gln Glu Gln Tyr 355 360 365	1104
gaa tta tac tgt gag atg ggc tcc aca ttc caa cta tgt aaa ata tgt Glu Leu Tyr Cys Glu Met Gly Ser Thr Phe Gln Leu Cys Lys Ile Cys 370 375 380	1152
gct gaa aat gat aag gat gta aag att gag ccc tgt gga cac ctc atg Ala Glu Asn Asp Lys Asp Val Lys Ile Glu Pro Cys Gly His Leu Met 385 390 395 400	1200
tgc aca tcc tgt ctt aca tcc tgg cag gaa tca gaa ggt cag ggc tgt Cys Thr Ser Cys Leu Thr Ser Trp Gln Glu Ser Glu Gly Gln Gly Cys 405 410 415	1248
cct ttc tgc cga tgt gaa att aaa ggt act gaa ccc atc gtg gta gat Pro Phe Cys Arg Cys Glu Ile Lys Gly Thr Glu Pro Ile Val Val Asp 420 425 430	1296
ccg ttt gat cct aga ggg agt ggc agc ctg ttg agg caa gga gca gag Pro Phe Asp Pro Arg Gly Ser Gly Ser Leu Leu Arg Gln Gly Ala Glu 435 440 445	1344

gga gct ccc tcc cca aat tat gat gat gat gat gat gaa cga gct gat Gly Ala Pro Ser Pro Asn Tyr Asp Asp Asp Asp Asp Glu Arg Ala Asp 450 455 460	1392
gat act ctc ttc atg atg aag gaa ttg gct ggt gcc aag gtg gaa cgg Asp Thr Leu Phe Met Met Lys Glu Leu Ala Gly Ala Lys Val Glu Arg 465 470 475 480	1440
ccg cct tct cca ttc tcc atg gcc cca caa gct tcc ctt ccc ccg gtg Pro Pro Ser Pro Phe Ser Met Ala Pro Gln Ala Ser Leu Pro Pro Val 485 490 495	1488
cca cca cga ctt gac ctt ctg ccg cag cga gta tgt gtt ccc tca agt Pro Pro Arg Leu Asp Leu Leu Pro Gln Arg Val Cys Val Pro Ser Ser 500 505 510	1536
gct tct gct ctt gga act gct tct aag gct gct tct ggc tcc ctt cat Ala Ser Ala Leu Gly Thr Ala Ser Lys Ala Ala Ser Gly Ser Leu His 515 520 525	1584
aaa gac aaa cca ttg cca gta cct ccc aca ctt cga gat ctt cca cca Lys Asp Lys Pro Leu Pro Val Pro Pro Thr Leu Arg Asp Leu Pro Pro 530 535 540	1632
cca ccg cct cca gac cgg cca tat tct gtt gga gca gaa tcc cga cct Pro Pro Pro Pro Asp Arg Pro Tyr Ser Val Gly Ala Glu Ser Arg Pro 545 550 555 560	1680
caa aga cgc ccc ttg cct tgt aca cca ggc gac tgt ccc tcc aga gac Gln Arg Arg Pro Leu Pro Cys Thr Pro Gly Asp Cys Pro Ser Arg Asp 565 570 575	1728
aaa ctg ccc cct gtc ccc tct agc cgc ctt gga gac tca tgg ctg ccc Lys Leu Pro Pro Val Pro Ser Ser Arg Leu Gly Asp Ser Trp Leu Pro 580 585 590	1776
cgg cca atc ccc aaa gta cca gta tct gcc cca agt tcc agt gat ccc Arg Pro Ile Pro Lys Val Pro Val Ser Ala Pro Ser Ser Ser Asp Pro 595 600 605	1824
tgg aca gga aga gaa tta acc aac cgg cac tca ctt cca ttt tca ttg Trp Thr Gly Arg Glu Leu Thr Asn Arg His Ser Leu Pro Phe Ser Leu 610 615 620	1872
ccc tca caa atg gag ccc aga cca gat gtg cct agg ctc gga agc acg Pro Ser Gln Met Glu Pro Arg Pro Asp Val Pro Arg Leu Gly Ser Thr 625 630 635 640	1920
ttc agt ctg gat acc tcc atg agt atg aat agc agc cca tta gta ggt Phe Ser Leu Asp Thr Ser Met Ser Met Asn Ser Ser Pro Leu Val Gly 645 650 655	1968
cca gag tgt gac cac ccc aaa atc aaa cct tcc tca tct gcc aat gcc Pro Glu Cys Asp His Pro Lys Ile Lys Pro Ser Ser Ser Ala Asn Ala 660 665 670	2016
att tat tct ctg gct gcc aga cct ctt cct gtg cca aaa ctg cca cct Ile Tyr Ser Leu Ala Ala Arg Pro Leu Pro Val Pro Lys Leu Pro Pro 675 680 685	2064
ggg gag caa tgt gag ggt gaa gag gac aca gag tac atg act ccc tct	2112

Gly	Glu	Gln	Cys	Glu	Gly	Glu	Glu	Asp	Thr	Glu	Tyr	Met	Thr	Pro	Ser		
690						695					700						
tcc	agg	cct	cta	cgg	cct	ttg	gat	aca	tcc	cag	agt	tca	cga	gca	tgt		2160
Ser	Arg	Pro	Leu	Arg	Pro	Leu	Asp	Thr	Ser	Gln	Ser	Ser	Arg	Ala	Cys		
705					710					715					720		
gat	tgc	gac	cag	cag	att	gat	agc	tgt	acg	tat	gaa	gca	atg	tat	aat		2208
Asp	Cys	Asp	Gln	Gln	Ile	Asp	Ser	Cys	Thr	Tyr	Glu	Ala	Met	Tyr	Asn		
				725					730					735			
att	cag	tcc	cag	gcg	cca	tct	atc	acc	gag	agc	agc	acc	ttt	ggg	gaa		2256
Ile	Gln	Ser	Gln	Ala	Pro	Ser	Ile	Thr	Glu	Ser	Ser	Thr	Phe	Gly	Glu		
			740					745						750			
ggg	aat	ttg	gcc	gca	gcc	cat	gcc	aac	act	ggg	ccc	gag	gag	tca	gaa		2304
Gly	Asn	Leu	Ala	Ala	Ala	His	Ala	Asn	Thr	Gly	Pro	Glu	Glu	Ser	Glu		
		755					760							765			
aat	gag	gat	gat	ggg	tat	gat	gtc	cca	aag	cca	cct	gtg	ccg	gcc	gtg		2352
Asn	Glu	Asp	Asp	Gly	Tyr	Asp	Val	Pro	Lys	Pro	Pro	Val	Pro	Ala	Val		
	770					775					780						
ctg	gcc	cgc	cga	act	ctc	tca	gat	atc	tct	aat	gcc	agc	tcc	tcc	ttt		2400
Leu	Ala	Arg	Arg	Thr	Leu	Ser	Asp	Ile	Ser	Asn	Ala	Ser	Ser	Ser	Phe		
785					790					795					800		
ggc	tgg	ttg	tct	ctg	gat	ggg	gat	cct	aca	aca	aat	gtc	act	gaa	ggg		2448
Gly	Trp	Leu	Ser	Leu	Asp	Gly	Asp	Pro	Thr	Thr	Asn	Val	Thr	Glu	Gly		
				805					810					815			
tcc	caa	gtt	ccc	gag	agg	cct	cca	aaa	cca	ttc	ccg	cgg	aga	atc	aac		2496
Ser	Gln	Val	Pro	Glu	Arg	Pro	Pro	Lys	Pro	Phe	Pro	Arg	Arg	Ile	Asn		
			820					825					830				
tct	gaa	cgg	aaa	gct	ggc	agc	tgt	cag	caa	ggg	agt	ggg	cct	gcc	gcc		2544
Ser	Glu	Arg	Lys	Ala	Gly	Ser	Cys	Gln	Gln	Gly	Ser	Gly	Pro	Ala	Ala		
		835					840					845					
tct	gct	gcc	acc	gcc	tca	cct	cag	ctc	tcc	agt	gag	atc	gag	aac	ctc		2592
Ser	Ala	Ala	Thr	Ala	Ser	Pro	Gln	Leu	Ser	Ser	Glu	Ile	Glu	Asn	Leu		
	850					855					860						
atg	agt	cag	ggg	tac	tcc	tac	cag	gac	atc	cag	aaa	gct	ttg	gtc	att		2640
Met	Ser	Gln	Gly	Tyr	Ser	Tyr	Gln	Asp	Ile	Gln	Lys	Ala	Leu	Val	Ile		
865					870					875					880		
gcc	cag	aac	aac	atc	gag	atg	gcc	aaa	aac	atc	ctc	cgg	gaa	ttt	gtt		2688
Ala	Gln	Asn	Asn	Ile	Glu	Met	Ala	Lys	Asn	Ile	Leu	Arg	Glu	Phe	Val		
			885						890					895			
tcc	att	tct	tct	cct	gcc	cat	gta	gct	acc	tag							2721
Ser	Ile	Ser	Ser	Pro	Ala	His	Val	Ala	Thr								
			900					905									

<210> 248

<211> 906

<212> PRT

<213> c-Cbl G306E

<400> 248

Met Ala Gly Asn Val Lys Lys Ser Ser Gly Ala Gly Gly Gly Thr Gly
 1 5 10 15

Ser Gly Gly Ser Gly Ser Gly Gly Leu Ile Gly Leu Met Lys Asp Ala
 20 25 30

Phe Gln Pro His His His His His His His Leu Ser Pro His Pro Pro
 35 40 45

Gly Thr Val Asp Lys Lys Met Val Glu Lys Cys Trp Lys Leu Met Asp
 50 55 60

Lys Val Val Arg Leu Cys Gln Asn Pro Lys Leu Ala Leu Lys Asn Ser
 65 70 75 80

Pro Pro Tyr Ile Leu Asp Leu Leu Pro Asp Thr Tyr Gln His Leu Arg
 85 90 95

Thr Ile Leu Ser Arg Tyr Glu Gly Lys Met Glu Thr Leu Gly Glu Asn
 100 105 110

Glu Tyr Phe Arg Val Phe Met Glu Asn Leu Met Lys Lys Thr Lys Gln
 115 120 125

Thr Ile Ser Leu Phe Lys Glu Gly Lys Glu Arg Met Tyr Glu Glu Asn
 130 135 140

Ser Gln Pro Arg Arg Asn Leu Thr Lys Leu Ser Leu Ile Phe Ser His
 145 150 155 160

Met Leu Ala Glu Leu Lys Gly Ile Phe Pro Ser Gly Leu Phe Gln Gly
 165 170 175

Asp Thr Phe Arg Ile Thr Lys Ala Asp Ala Ala Glu Phe Trp Arg Lys
 180 185 190

Ala Phe Gly Glu Lys Thr Ile Val Pro Trp Lys Ser Phe Arg Gln Ala
 195 200 205

Leu His Glu Val His Pro Ile Ser Ser Gly Leu Glu Ala Met Ala Leu
 210 215 220

Lys Ser Thr Ile Asp Leu Thr Cys Asn Asp Tyr Ile Ser Val Phe Glu
 225 230 235 240

Phe Asp Ile Phe Thr Arg Leu Phe Gln Pro Trp Ser Ser Leu Leu Arg
 245 250 255

Asn Trp Asn Ser Leu Ala Val Thr His Pro Gly Tyr Met Ala Phe Leu
 260 265 270

Thr Tyr Asp Glu Val Lys Ala Arg Leu Gln Lys Phe Ile His Lys Pro
 275 280 285

Gly Ser Tyr Ile Phe Arg Leu Ser Cys Thr Arg Leu Gly Gln Trp Ala

290	295	300
Ile Glu Tyr Val Thr Ala Asp Gly Asn Ile Leu Gln Thr Ile Pro His 305 310 315 320		
Asn Lys Pro Leu Phe Gln Ala Leu Ile Asp Gly Phe Arg Glu Gly Phe 325 330 335		
Tyr Leu Phe Pro Asp Gly Arg Asn Gln Asn Pro Asp Leu Thr Gly Leu 340 345 350		
Cys Glu Pro Thr Pro Gln Asp His Ile Lys Val Thr Gln Glu Gln Tyr 355 360 365		
Glu Leu Tyr Cys Glu Met Gly Ser Thr Phe Gln Leu Cys Lys Ile Cys 370 375 380		
Ala Glu Asn Asp Lys Asp Val Lys Ile Glu Pro Cys Gly His Leu Met 385 390 395 400		
Cys Thr Ser Cys Leu Thr Ser Trp Gln Glu Ser Glu Gly Gln Gly Cys 405 410 415		
Pro Phe Cys Arg Cys Glu Ile Lys Gly Thr Glu Pro Ile Val Val Asp 420 425 430		
Pro Phe Asp Pro Arg Gly Ser Gly Ser Leu Leu Arg Gln Gly Ala Glu 435 440 445		
Gly Ala Pro Ser Pro Asn Tyr Asp Asp Asp Asp Glu Arg Ala Asp 450 455 460		
Asp Thr Leu Phe Met Met Lys Glu Leu Ala Gly Ala Lys Val Glu Arg 465 470 475 480		
Pro Pro Ser Pro Phe Ser Met Ala Pro Gln Ala Ser Leu Pro Pro Val 485 490 495		
Pro Pro Arg Leu Asp Leu Leu Pro Gln Arg Val Cys Val Pro Ser Ser 500 505 510		
Ala Ser Ala Leu Gly Thr Ala Ser Lys Ala Ala Ser Gly Ser Leu His 515 520 525		
Lys Asp Lys Pro Leu Pro Val Pro Pro Thr Leu Arg Asp Leu Pro Pro 530 535 540		
Pro Pro Pro Pro Asp Arg Pro Tyr Ser Val Gly Ala Glu Ser Arg Pro 545 550 555 560		
Gln Arg Arg Pro Leu Pro Cys Thr Pro Gly Asp Cys Pro Ser Arg Asp 565 570 575		
Lys Leu Pro Pro Val Pro Ser Ser Arg Leu Gly Asp Ser Trp Leu Pro 580 585 590		
Arg Pro Ile Pro Lys Val Pro Val Ser Ala Pro Ser Ser Ser Asp Pro 595 600 605		
Trp Thr Gly Arg Glu Leu Thr Asn Arg His Ser Leu Pro Phe Ser Leu 610 615 620		

Pro Ser Gln Met Glu Pro Arg Pro Asp Val Pro Arg Leu Gly Ser Thr
625 630 635 640

Phe Ser Leu Asp Thr Ser Met Ser Met Asn Ser Ser Pro Leu Val Gly
645 650 655

Pro Glu Cys Asp His Pro Lys Ile Lys Pro Ser Ser Ser Ala Asn Ala
660 665 670

Ile Tyr Ser Leu Ala Ala Arg Pro Leu Pro Val Pro Lys Leu Pro Pro
675 680 685

Gly Glu Gln Cys Glu Gly Glu Glu Asp Thr Glu Tyr Met Thr Pro Ser
690 695 700

Ser Arg Pro Leu Arg Pro Leu Asp Thr Ser Gln Ser Ser Arg Ala Cys
705 710 715 720

Asp Cys Asp Gln Gln Ile Asp Ser Cys Thr Tyr Glu Ala Met Tyr Asn
725 730 735

Ile Gln Ser Gln Ala Pro Ser Ile Thr Glu Ser Ser Thr Phe Gly Glu
740 745 750

Gly Asn Leu Ala Ala Ala His Ala Asn Thr Gly Pro Glu Glu Ser Glu
755 760 765

Asn Glu Asp Asp Gly Tyr Asp Val Pro Lys Pro Pro Val Pro Ala Val
770 775 780

Leu Ala Arg Arg Thr Leu Ser Asp Ile Ser Asn Ala Ser Ser Ser Phe
785 790 795 800

Gly Trp Leu Ser Leu Asp Gly Asp Pro Thr Thr Asn Val Thr Glu Gly
805 810 815

Ser Gln Val Pro Glu Arg Pro Pro Lys Pro Phe Pro Arg Arg Ile Asn
820 825 830

Ser Glu Arg Lys Ala Gly Ser Cys Gln Gln Gly Ser Gly Pro Ala Ala
835 840 845

Ser Ala Ala Thr Ala Ser Pro Gln Leu Ser Ser Glu Ile Glu Asn Leu
850 855 860

Met Ser Gln Gly Tyr Ser Tyr Gln Asp Ile Gln Lys Ala Leu Val Ile
865 870 875 880

Ala Gln Asn Asn Ile Glu Met Ala Lys Asn Ile Leu Arg Glu Phe Val
885 890 895

Ser Ile Ser Ser Pro Ala His Val Ala Thr
900 905

<210> 249

<211> 2721

<212> DNA

<213> c-Cbl C381A

<220>

<221> CDS

<222> (1) .. (2718)

<223>

<400> 249

atg gcc ggc aac gtg aag aag agc tct ggg gcc ggg ggc ggc acg ggc	48
Met Ala Gly Asn Val Lys Lys Ser Ser Gly Ala Gly Gly Gly Thr Gly	
1 5 10 15	

tcc ggg ggc tcc ggt tcc ggt ggc ctg att ggg ctc atg aag gac gcc	96
Ser Gly Gly Ser Gly Ser Gly Gly Leu Ile Gly Leu Met Lys Asp Ala	
20 25 30	

ttc cag ccg cac cac cac cac cac cac ctc agc ccc cac ccg ccg	144
Phe Gln Pro His His His His His His His Leu Ser Pro His Pro Pro	
35 40 45	

ggg acg gtg gac aag aag atg gtg gag aag tgc tgg aag ctc atg gac	192
Gly Thr Val Asp Lys Lys Met Val Glu Lys Cys Trp Lys Leu Met Asp	
50 55 60	

aag gtg gtg cgg ttg tgt cag aac cca aag ctg gcg cta aag aat agc	240
Lys Val Val Arg Leu Cys Gln Asn Pro Lys Leu Ala Leu Lys Asn Ser	
65 70 75 80	

cca cct tat atc tta gac ctg cta cca gat acc tac cag cat ctc cgt	288
Pro Pro Tyr Ile Leu Asp Leu Leu Pro Asp Thr Tyr Gln His Leu Arg	
85 90 95	

act atc ttg tca aga tat gag ggg aag atg gag aca ctt gga gaa aat	336
Thr Ile Leu Ser Arg Tyr Glu Gly Lys Met Glu Thr Leu Gly Glu Asn	
100 105 110	

gag tat ttt agg gtg ttt atg gag aat ttg atg aag aaa act aag caa	384
Glu Tyr Phe Arg Val Phe Met Glu Asn Leu Met Lys Lys Thr Lys Gln	
115 120 125	

acc ata agc ctc ttc aag gag gga aaa gaa aga atg tat gag gag aat	432
Thr Ile Ser Leu Phe Lys Glu Gly Lys Glu Arg Met Tyr Glu Glu Asn	
130 135 140	

tct cag cct agg cga aac cta acc aaa ctg tcc ctc atc ttc agc cac	480
Ser Gln Pro Arg Arg Asn Leu Thr Lys Leu Ser Leu Ile Phe Ser His	
145 150 155 160	

atg ctg gca gaa cta aaa gga atc ttt cca agt gga ctc ttt cag gga	528
Met Leu Ala Glu Leu Lys Gly Ile Phe Pro Ser Gly Leu Phe Gln Gly	
165 170 175	

gac aca ttt cgg att act aaa gca gat gct gcg gaa ttt tgg aga aaa	576
Asp Thr Phe Arg Ile Thr Lys Ala Asp Ala Ala Glu Phe Trp Arg Lys	

180	185	190	
gct ttt ggg gaa aag aca ata gtc cct tgg aag agc ttt cga cag gct Ala Phe Gly Glu Lys Thr Ile Val Pro Trp Lys Ser Phe Arg Gln Ala 195 200 205			624
cta cat gaa gtg cat ccc atc agt tct ggg ctg gag gcc atg gct ctg Leu His Glu Val His Pro Ile Ser Ser Gly Leu Glu Ala Met Ala Leu 210 215 220			672
aaa tcc act att gat ctg acc tgc aat gat tat att tcg gtt ttt gaa Lys Ser Thr Ile Asp Leu Thr Cys Asn Asp Tyr Ile Ser Val Phe Glu 225 230 235 240			720
ttt gac atc ttt acc cga ctc ttt cag ccc tgg tcc tct ttg ctc agg Phe Asp Ile Phe Thr Arg Leu Phe Gln Pro Trp Ser Ser Leu Leu Arg 245 250 255			768
aat tgg aac agc ctt gct gta act cat cct ggc tac atg gct ttt ttg Asn Trp Asn Ser Leu Ala Val Thr His Pro Gly Tyr Met Ala Phe Leu 260 265 270			816
acg tat gac gaa gtg aaa gct cgg ctc cag aaa ttc att cac aaa cct Thr Tyr Asp Glu Val Lys Ala Arg Leu Gln Lys Phe Ile His Lys Pro 275 280 285			864
ggc agt tat atc ttc cgg ctg agc tgt act cgt ctg ggt cag tgg gct Gly Ser Tyr Ile Phe Arg Leu Ser Cys Thr Arg Leu Gly Gln Trp Ala 290 295 300			912
att ggg tat gtt act gct gat ggg aac att ctc cag aca atc cct cac Ile Gly Tyr Val Thr Ala Asp Gly Asn Ile Leu Gln Thr Ile Pro His 305 310 315 320			960
aat aaa cct ctc ttc caa gca ctg att gat ggc ttc agg gaa ggc ttc Asn Lys Pro Leu Phe Gln Ala Leu Ile Asp Gly Phe Arg Glu Gly Phe 325 330 335			1008
tat ttg ttt cct gat gga cga aat cag aat cct gat ctg act ggc tta Tyr Leu Phe Pro Asp Gly Arg Asn Gln Asn Pro Asp Leu Thr Gly Leu 340 345 350			1056
tgt gaa cca act ccc caa gac cat atc aaa gtg acc cag gaa caa tat Cys Glu Pro Thr Pro Gln Asp His Ile Lys Val Thr Gln Glu Gln Tyr 355 360 365			1104
gaa tta tac tgt gag atg ggc tcc aca ttc caa cta gct aaa ata tgt Glu Leu Tyr Cys Glu Met Gly Ser Thr Phe Gln Leu Ala Lys Ile Cys 370 375 380			1152
gct gaa aat gat aag gat gta aag att gag ccc tgt gga cac ctc atg Ala Glu Asn Asp Lys Asp Val Lys Ile Glu Pro Cys Gly His Leu Met 385 390 395 400			1200
tgc aca tcc tgt ctt aca tcc tgg cag gaa tca gaa ggt cag ggc tgt Cys Thr Ser Cys Leu Thr Ser Trp Gln Glu Ser Glu Gly Gln Gly Cys 405 410 415			1248
cct ttc tgc cga tgt gaa att aaa ggt act gaa ccc atc gtg gta gat Pro Phe Cys Arg Cys Glu Ile Lys Gly Thr Glu Pro Ile Val Val Asp 420 425 430			1296

ccg ttt gat cct aga ggg agt ggc agc ctg ttg agg caa gga gca gag Pro Phe Asp Pro Arg Gly Ser Gly Ser Leu Leu Arg Gln Gly Ala Glu 435 440 445	1344
gga gct ccc tcc cca aat tat gat gat gat gat gat gaa cga gct gat Gly Ala Pro Ser Pro Asn Tyr Asp Asp Asp Asp Asp Glu Arg Ala Asp 450 455 460	1392
gat act ctc ttc atg atg aag gaa ttg gct ggt gcc aag gtg gaa cgg Asp Thr Leu Phe Met Met Lys Glu Leu Ala Gly Ala Lys Val Glu Arg 465 470 475 480	1440
ccg cct tct cca ttc tcc atg gcc cca caa gct tcc ctt ccc ccg gtg Pro Pro Ser Pro Phe Ser Met Ala Pro Gln Ala Ser Leu Pro Pro Val 485 490 495	1488
cca cca cga ctt gac ctt ctg ccg cag cga gta tgt gtt ccc tca agt Pro Pro Arg Leu Asp Leu Leu Pro Gln Arg Val Cys Val Pro Ser Ser 500 505 510	1536
gct tct gct ctt gga act gct tct aag gct gct tct ggc tcc ctt cat Ala Ser Ala Leu Gly Thr Ala Ser Lys Ala Ala Ser Gly Ser Leu His 515 520 525	1584
aaa gac aaa cca ttg cca gta cct ccc aca ctt cga gat ctt cca cca Lys Asp Lys Pro Leu Pro Val Pro Pro Thr Leu Arg Asp Leu Pro Pro 530 535 540	1632
cca ccg cct cca gac cgg cca tat tct gtt gga gca gaa tcc cga cct Pro Pro Pro Pro Asp Arg Pro Tyr Ser Val Gly Ala Glu Ser Arg Pro 545 550 555 560	1680
caa aga cgc ccc ttg cct tgt aca cca ggc gac tgt ccc tcc aga gac Gln Arg Arg Pro Leu Pro Cys Thr Pro Gly Asp Cys Pro Ser Arg Asp 565 570 575	1728
aaa ctg ccc cct gtc ccc tct agc cgc ctt gga gac tca tgg ctg ccc Lys Leu Pro Pro Val Pro Ser Ser Arg Leu Gly Asp Ser Trp Leu Pro 580 585 590	1776
cgg cca atc ccc aaa gta cca gta tct gcc cca agt tcc agt gat ccc Arg Pro Ile Pro Lys Val Pro Val Ser Ala Pro Ser Ser Ser Asp Pro 595 600 605	1824
tgg aca gga aga gaa tta acc aac cgg cac tca ctt cca ttt tca ttg Trp Thr Gly Arg Glu Leu Thr Asn Arg His Ser Leu Pro Phe Ser Leu 610 615 620	1872
ccc tca caa atg gag ccc aga cca gat gtg cct agg ctc gga agc acg Pro Ser Gln Met Glu Pro Arg Pro Asp Val Pro Arg Leu Gly Ser Thr 625 630 635 640	1920
ttc agt ctg gat acc tcc atg agt atg aat agc agc cca tta gta ggt Phe Ser Leu Asp Thr Ser Met Ser Met Asn Ser Ser Pro Leu Val Gly 645 650 655	1968
cca gag tgt gac cac ccc aaa atc aaa cct tcc tca tct gcc aat gcc Pro Glu Cys Asp His Pro Lys Ile Lys Pro Ser Ser Ser Ala Asn Ala 660 665 670	2016

att tat tct ctg gct gcc aga cct ctt cct gtg cca aaa ctg cca cct Ile Tyr Ser Leu Ala Ala Arg Pro Leu Pro Val Pro Lys Leu Pro Pro 675 680 685	2064
ggg gag caa tgt gag ggt gaa gag gac aca gag tac atg act ccc tct Gly Glu Gln Cys Glu Gly Glu Asp Thr Glu Tyr Met Thr Pro Ser 690 695 700	2112
tcc agg cct cta cgg cct ttg gat aca tcc cag agt tca cga gca tgt Ser Arg Pro Leu Arg Pro Leu Asp Thr Ser Gln Ser Ser Arg Ala Cys 705 710 715 720	2160
gat tgc gac cag cag att gat agc tgt acg tat gaa gca atg tat aat Asp Cys Asp Gln Gln Ile Asp Ser Cys Thr Tyr Glu Ala Met Tyr Asn 725 730 735	2208
att cag tcc cag gcg cca tct atc acc gag agc agc acc ttt ggt gaa Ile Gln Ser Gln Ala Pro Ser Ile Thr Glu Ser Ser Thr Phe Gly Glu 740 745 750	2256
ggg aat ttg gcc gca gcc cat gcc aac act ggt ccc gag gag tca gaa Gly Asn Leu Ala Ala Ala His Ala Asn Thr Gly Pro Glu Glu Ser Glu 755 760 765	2304
aat gag gat gat ggg tat gat gtc cca aag cca cct gtg ccg gcc gtg Asn Glu Asp Asp Gly Tyr Asp Val Pro Lys Pro Pro Val Pro Ala Val 770 775 780	2352
ctg gcc cgc cga act ctc tca gat atc tct aat gcc agc tcc tcc ttt Leu Ala Arg Arg Thr Leu Ser Asp Ile Ser Asn Ala Ser Ser Ser Phe 785 790 795 800	2400
ggc tgg ttg tct ctg gat ggt gat cct aca aca aat gtc act gaa ggt Gly Trp Leu Ser Leu Asp Gly Asp Pro Thr Asn Val Thr Glu Gly 805 810 815	2448
tcc caa gtt ccc gag agg cct cca aaa cca ttc ccg cgg aga atc aac Ser Gln Val Pro Glu Arg Pro Pro Lys Pro Phe Pro Arg Arg Ile Asn 820 825 830	2496
tct gaa cgg aaa gct ggc agc tgt cag caa ggt agt ggt cct gcc gcc Ser Glu Arg Lys Ala Gly Ser Cys Gln Gln Gly Ser Gly Pro Ala Ala 835 840 845	2544
tct gct gcc acc gcc tca cct cag ctc tcc agt gag atc gag aac ctc Ser Ala Ala Thr Ala Ser Pro Gln Leu Ser Ser Glu Ile Glu Asn Leu 850 855 860	2592
atg agt cag ggg tac tcc tac cag gac atc cag aaa gct ttg gtc att Met Ser Gln Gly Tyr Ser Tyr Gln Asp Ile Gln Lys Ala Leu Val Ile 865 870 875 880	2640
gcc cag aac aac atc gag atg gcc aaa aac atc ctc cgg gaa ttt gtt Ala Gln Asn Asn Ile Glu Met Ala Lys Asn Ile Leu Arg Glu Phe Val 885 890 895	2688
tcc att tct tct cct gcc cat gta gct acc tag Ser Ile Ser Ser Pro Ala His Val Ala Thr 900 905	2721

<210> 250

<211> 906

<212> PRT

<213> c-Cbl C381A

<400> 250

Met Ala Gly Asn Val Lys Lys Ser Ser Gly Ala Gly Gly Gly Thr Gly
1 5 10 15

Ser Gly Gly Ser Gly Ser Gly Gly Leu Ile Gly Leu Met Lys Asp Ala
20 25 30

Phe Gln Pro His His His His His His His Leu Ser Pro His Pro Pro
35 40 45

Gly Thr Val Asp Lys Lys Met Val Glu Lys Cys Trp Lys Leu Met Asp
50 55 60

Lys Val Val Arg Leu Cys Gln Asn Pro Lys Leu Ala Leu Lys Asn Ser
65 70 75 80

Pro Pro Tyr Ile Leu Asp Leu Leu Pro Asp Thr Tyr Gln His Leu Arg
85 90 95

Thr Ile Leu Ser Arg Tyr Glu Gly Lys Met Glu Thr Leu Gly Glu Asn
100 105 110

Glu Tyr Phe Arg Val Phe Met Glu Asn Leu Met Lys Lys Thr Lys Gln
115 120 125

Thr Ile Ser Leu Phe Lys Glu Gly Lys Glu Arg Met Tyr Glu Glu Asn
130 135 140

Ser Gln Pro Arg Arg Asn Leu Thr Lys Leu Ser Leu Ile Phe Ser His
145 150 155 160

Met Leu Ala Glu Leu Lys Gly Ile Phe Pro Ser Gly Leu Phe Gln Gly
165 170 175

Asp Thr Phe Arg Ile Thr Lys Ala Asp Ala Ala Glu Phe Trp Arg Lys
180 185 190

Ala Phe Gly Glu Lys Thr Ile Val Pro Trp Lys Ser Phe Arg Gln Ala
195 200 205

Leu His Glu Val His Pro Ile Ser Ser Gly Leu Glu Ala Met Ala Leu
210 215 220

Lys Ser Thr Ile Asp Leu Thr Cys Asn Asp Tyr Ile Ser Val Phe Glu
225 230 235 240

Phe Asp Ile Phe Thr Arg Leu Phe Gln Pro Trp Ser Ser Leu Leu Arg
245 250 255

Asn Trp Asn Ser Leu Ala Val Thr His Pro Gly Tyr Met Ala Phe Leu
 260 265 270
 Thr Tyr Asp Glu Val Lys Ala Arg Leu Gln Lys Phe Ile His Lys Pro
 275 280 285
 Gly Ser Tyr Ile Phe Arg Leu Ser Cys Thr Arg Leu Gly Gln Trp Ala
 290 295 300
 Ile Gly Tyr Val Thr Ala Asp Gly Asn Ile Leu Gln Thr Ile Pro His
 305 310 315 320
 Asn Lys Pro Leu Phe Gln Ala Leu Ile Asp Gly Phe Arg Glu Gly Phe
 325 330 335
 Tyr Leu Phe Pro Asp Gly Arg Asn Gln Asn Pro Asp Leu Thr Gly Leu
 340 345 350
 Cys Glu Pro Thr Pro Gln Asp His Ile Lys Val Thr Gln Glu Gln Tyr
 355 360 365
 Glu Leu Tyr Cys Glu Met Gly Ser Thr Phe Gln Leu Ala Lys Ile Cys
 370 375 380
 Ala Glu Asn Asp Lys Asp Val Lys Ile Glu Pro Cys Gly His Leu Met
 385 390 395 400
 Cys Thr Ser Cys Leu Thr Ser Trp Gln Glu Ser Glu Gly Gln Gly Cys
 405 410 415
 Pro Phe Cys Arg Cys Glu Ile Lys Gly Thr Glu Pro Ile Val Val Asp
 420 425 430
 Pro Phe Asp Pro Arg Gly Ser Gly Ser Leu Leu Arg Gln Gly Ala Glu
 435 440 445
 Gly Ala Pro Ser Pro Asn Tyr Asp Asp Asp Asp Asp Glu Arg Ala Asp
 450 455 460
 Asp Thr Leu Phe Met Met Lys Glu Leu Ala Gly Ala Lys Val Glu Arg
 465 470 475 480
 Pro Pro Ser Pro Phe Ser Met Ala Pro Gln Ala Ser Leu Pro Pro Val
 485 490 495
 Pro Pro Arg Leu Asp Leu Leu Pro Gln Arg Val Cys Val Pro Ser Ser
 500 505 510
 Ala Ser Ala Leu Gly Thr Ala Ser Lys Ala Ala Ser Gly Ser Leu His
 515 520 525
 Lys Asp Lys Pro Leu Pro Val Pro Pro Thr Leu Arg Asp Leu Pro Pro
 530 535 540
 Pro Pro Pro Pro Asp Arg Pro Tyr Ser Val Gly Ala Glu Ser Arg Pro
 545 550 555 560
 Gln Arg Arg Pro Leu Pro Cys Thr Pro Gly Asp Cys Pro Ser Arg Asp
 565 570 575
 Lys Leu Pro Pro Val Pro Ser Ser Arg Leu Gly Asp Ser Trp Leu Pro

580					585					590						
Arg	Pro	Ile	Pro	Lys	Val	Pro	Val	Ser	Ala	Pro	Ser	Ser	Ser	Asp	Pro	
595					600					605						
Trp	Thr	Gly	Arg	Glu	Leu	Thr	Asn	Arg	His	Ser	Leu	Pro	Phe	Ser	Leu	
610					615					620						
Pro	Ser	Gln	Met	Glu	Pro	Arg	Pro	Asp	Val	Pro	Arg	Leu	Gly	Ser	Thr	
625					630					635					640	
Phe	Ser	Leu	Asp	Thr	Ser	Met	Ser	Met	Asn	Ser	Ser	Pro	Leu	Val	Gly	
645					650					655						
Pro	Glu	Cys	Asp	His	Pro	Lys	Ile	Lys	Pro	Ser	Ser	Ser	Ala	Asn	Ala	
660					665					670						
Ile	Tyr	Ser	Leu	Ala	Ala	Arg	Pro	Leu	Pro	Val	Pro	Lys	Leu	Pro	Pro	
675					680					685						
Gly	Glu	Gln	Cys	Glu	Gly	Glu	Glu	Asp	Thr	Glu	Tyr	Met	Thr	Pro	Ser	
690					695					700						
Ser	Arg	Pro	Leu	Arg	Pro	Leu	Asp	Thr	Ser	Gln	Ser	Ser	Arg	Ala	Cys	
705					710					715					720	
Asp	Cys	Asp	Gln	Gln	Ile	Asp	Ser	Cys	Thr	Tyr	Glu	Ala	Met	Tyr	Asn	
725					730					735						
Ile	Gln	Ser	Gln	Ala	Pro	Ser	Ile	Thr	Glu	Ser	Ser	Thr	Phe	Gly	Glu	
740					745					750						
Gly	Asn	Leu	Ala	Ala	Ala	His	Ala	Asn	Thr	Gly	Pro	Glu	Glu	Ser	Glu	
755					760					765						
Asn	Glu	Asp	Asp	Gly	Tyr	Asp	Val	Pro	Lys	Pro	Pro	Val	Pro	Ala	Val	
770					775					780						
Leu	Ala	Arg	Arg	Thr	Leu	Ser	Asp	Ile	Ser	Asn	Ala	Ser	Ser	Ser	Phe	
785					790					795					800	
Gly	Trp	Leu	Ser	Leu	Asp	Gly	Asp	Pro	Thr	Thr	Asn	Val	Thr	Glu	Gly	
805					810					815						
Ser	Gln	Val	Pro	Glu	Arg	Pro	Pro	Lys	Pro	Phe	Pro	Arg	Arg	Ile	Asn	
820					825					830						
Ser	Glu	Arg	Lys	Ala	Gly	Ser	Cys	Gln	Gln	Gly	Ser	Gly	Pro	Ala	Ala	
835					840					845						
Ser	Ala	Ala	Thr	Ala	Ser	Pro	Gln	Leu	Ser	Ser	Glu	Ile	Glu	Asn	Leu	
850					855					860						
Met	Ser	Gln	Gly	Tyr	Ser	Tyr	Gln	Asp	Ile	Gln	Lys	Ala	Leu	Val	Ile	
865					870					875					880	
Ala	Gln	Asn	Asn	Ile	Glu	Met	Ala	Lys	Asn	Ile	Leu	Arg	Glu	Phe	Val	
885					890					895						
Ser	Ile	Ser	Ser	Pro	Ala	His	Val	Ala	Thr							

900

905

<210> 251

<211> 2721

<212> DNA

<213> c-Cbl Y700F

<220>

<221> CDS

<222> (1) .. (2718)

<223>

<400> 251

atg gcc ggc aac gtg aag aag agc tct ggg gcc ggg ggc ggc acg ggc	48
Met Ala Gly Asn Val Lys Lys Ser Ser Gly Ala Gly Gly Gly Thr Gly	
1 5 10 15	
tcc ggg ggc tcg ggt tcg ggt ggc ctg att ggg ctc atg aag gac gcc	96
Ser Gly Gly Ser Gly Ser Gly Gly Leu Ile Gly Leu Met Lys Asp Ala	
20 25 30	
ttc cag ccg cac cac cac cac cac cac ctc agc ccc cac ccg ccg	144
Phe Gln Pro His His His His His His His Leu Ser Pro His Pro Pro	
35 40 45	
ggg acg gtg gac aag aag atg gtg gag aag tgc tgg aag ctc atg gac	192
Gly Thr Val Asp Lys Lys Met Val Glu Lys Cys Trp Lys Leu Met Asp	
50 55 60	
aag gtg gtg cgg ttg tgt cag aac cca aag ctg gcg cta aag aat agc	240
Lys Val Val Arg Leu Cys Gln Asn Pro Lys Leu Ala Leu Lys Asn Ser	
65 70 75 80	
cca cct tat atc tta gac ctg cta cca gat acc tac cag cat ctc cgt	288
Pro Pro Tyr Ile Leu Asp Leu Leu Pro Asp Thr Tyr Gln His Leu Arg	
85 90 95	
act atc ttg tca aga tat gag ggg aag atg gag aca ctt gga gaa aat	336
Thr Ile Leu Ser Arg Tyr Glu Gly Lys Met Glu Thr Leu Gly Glu Asn	
100 105 110	
gag tat ttt agg gtg ttt atg gag aat ttg atg aag aaa act aag caa	384
Glu Tyr Phe Arg Val Phe Met Glu Asn Leu Met Lys Lys Thr Lys Gln	
115 120 125	
acc ata agc ctc ttc aag gag gga aaa gaa aga atg tat gag gag aat	432
Thr Ile Ser Leu Phe Lys Glu Gly Lys Glu Arg Met Tyr Glu Glu Asn	
130 135 140	
tct cag cct agg cga aac cta acc aaa ctg tcc ctc atc ttc agc cac	480
Ser Gln Pro Arg Arg Asn Leu Thr Lys Leu Ser Leu Ile Phe Ser His	

145	150	155	160	
atg ctg gca gaa cta aaa gga atc ttt cca agt gga ctc ttt cag gga				528
Met Leu Ala Glu Leu Lys Gly Ile Phe Pro Ser Gly Leu Phe Gln Gly	165	170	175	
gac aca ttt cgg att act aaa gca gat gct gcg gaa ttt tgg aga aaa				576
Asp Thr Phe Arg Ile Thr Lys Ala Asp Ala Ala Glu Phe Trp Arg Lys	180	185	190	
gct ttt ggg gaa aag aca ata gtc cct tgg aag agc ttt cga cag gct				624
Ala Phe Gly Glu Lys Thr Ile Val Pro Trp Lys Ser Phe Arg Gln Ala	195	200	205	
cta cat gaa gtg cat ccc atc agt tct ggg ctg gag gcc atg gct ctg				672
Leu His Glu Val His Pro Ile Ser Ser Gly Leu Glu Ala Met Ala Leu	210	215	220	
aaa tcc act att gat ctg acc tgc aat gat tat att tcg gtt ttt gaa				720
Lys Ser Thr Ile Asp Leu Thr Cys Asn Asp Tyr Ile Ser Val Phe Glu	225	230	235	240
ttt gac atc ttt acc cga ctc ttt cag ccc tgg tcc tct ttg ctc agg				768
Phe Asp Ile Phe Thr Arg Leu Phe Gln Pro Trp Ser Ser Leu Leu Arg	245	250	255	
aat tgg aac agc ctt gct gta act cat cct ggc tac atg gct ttt ttg				816
Asn Trp Asn Ser Leu Ala Val Thr His Pro Gly Tyr Met Ala Phe Leu	260	265	270	
acg tat gac gaa gtg aaa gct cgg ctc cag aaa ttc att cac aaa cct				864
Thr Tyr Asp Glu Val Lys Ala Arg Leu Gln Lys Phe Ile His Lys Pro	275	280	285	
ggc agt tat atc ttc cgg ctg agc tgt act cgt ctg ggt cag tgg gct				912
Gly Ser Tyr Ile Phe Arg Leu Ser Cys Thr Arg Leu Gly Gln Trp Ala	290	295	300	
att ggg tat gtt act gct gat ggg aac att ctc cag aca atc cct cac				960
Ile Gly Tyr Val Thr Ala Asp Gly Asn Ile Leu Gln Thr Ile Pro His	305	310	315	320
aat aaa cct ctc ttc caa gca ctg att gat ggc ttc agg gaa ggc ttc				1008
Asn Lys Pro Leu Phe Gln Ala Leu Ile Asp Gly Phe Arg Glu Gly Phe	325	330	335	
tat ttg ttt cct gat gga cga aat cag aat cct gat ctg act ggc tta				1056
Tyr Leu Phe Pro Asp Gly Arg Asn Gln Asn Pro Asp Leu Thr Gly Leu	340	345	350	
tgt gaa cca act ccc caa gac cat atc aaa gtg acc cag gaa caa tat				1104
Cys Glu Pro Thr Pro Gln Asp His Ile Lys Val Thr Gln Glu Gln Tyr	355	360	365	
gaa tta tac tgt gag atg ggc tcc aca ttc caa cta tgt aaa ata tgt				1152
Glu Leu Tyr Cys Glu Met Gly Ser Thr Phe Gln Leu Cys Lys Ile Cys	370	375	380	
gct gaa aat gat aag gat gta aag att gag ccc tgt gga cac ctc atg				1200
Ala Glu Asn Asp Lys Asp Val Lys Ile Glu Pro Cys Gly His Leu Met	385	390	395	400

tgc aca tcc tgt ctt aca tcc tgg cag gaa tca gaa ggt cag ggc tgt	1248
Cys Thr Ser Cys Leu Thr Ser Trp Gln Glu Ser Glu Gly Gln Gly Cys	
405 410 415	
cct ttc tgc cga tgt gaa att aaa ggt act gaa ccc atc gtg gta gat	1296
Pro Phe Cys Arg Cys Glu Ile Lys Gly Thr Glu Pro Ile Val Val Asp	
420 425 430	
ccg ttt gat cct aga ggg agt ggc agc ctg ttg agg caa gga gca gag	1344
Pro Phe Asp Pro Arg Gly Ser Gly Ser Leu Leu Arg Gln Gly Ala Glu	
435 440 445	
gga gct ccc tcc cca aat tat gat gat gat gat gat gaa cga gct gat	1392
Gly Ala Pro Ser Pro Asn Tyr Asp Asp Asp Asp Asp Glu Arg Ala Asp	
450 455 460	
gat act ctc ttc atg atg aag gaa ttg gct ggt gcc aag gtg gaa cgg	1440
Asp Thr Leu Phe Met Met Lys Glu Leu Ala Gly Ala Lys Val Glu Arg	
465 470 475 480	
ccg cct tct cca ttc tcc atg gcc cca caa gct tcc ctt ccc ccg gtg	1488
Pro Pro Ser Pro Phe Ser Met Ala Pro Gln Ala Ser Leu Pro Pro Val	
485 490 495	
cca cca cga ctt gac ctt ctg ccg cag cga gta tgt gtt ccc tca agt	1536
Pro Pro Arg Leu Asp Leu Leu Pro Gln Arg Val Cys Val Pro Ser Ser	
500 505 510	
gct tct gct ctt gga act gct tct aag gct gct tct ggc tcc ctt cat	1584
Ala Ser Ala Leu Gly Thr Ala Ser Lys Ala Ala Ser Gly Ser Leu His	
515 520 525	
aaa gac aaa cca ttg cca gta cct ccc aca ctt cga gat ctt cca cca	1632
Lys Asp Lys Pro Leu Pro Val Pro Pro Thr Leu Arg Asp Leu Pro Pro	
530 535 540	
cca ccg cct cca gac cgg cca tat tct gtt gga gca gaa tcc cga cct	1680
Pro Pro Pro Pro Asp Arg Pro Tyr Ser Val Gly Ala Glu Ser Arg Pro	
545 550 555 560	
caa aga cgc ccc ttg cct tgt aca cca ggc gac tgt ccc tcc aga gac	1728
Gln Arg Arg Pro Leu Pro Cys Thr Pro Gly Asp Cys Pro Ser Arg Asp	
565 570 575	
aaa ctg ccc cct gtc ccc tct agc cgc ctt gga gac tca tgg ctg ccc	1776
Lys Leu Pro Pro Val Pro Ser Ser Arg Leu Gly Asp Ser Trp Leu Pro	
580 585 590	
cgg cca atc ccc aaa gta cca gta tct gcc cca agt tcc agt gat ccc	1824
Arg Pro Ile Pro Lys Val Pro Val Ser Ala Pro Ser Ser Ser Asp Pro	
595 600 605	
tgg aca gga aga gaa tta acc aac cgg cac tca ctt cca ttt tca ttg	1872
Trp Thr Gly Arg Glu Leu Thr Asn Arg His Ser Leu Pro Phe Ser Leu	
610 615 620	
ccc tca caa atg gag ccc aga cca gat gtg cct agg ctc gga agc acg	1920
Pro Ser Gln Met Glu Pro Arg Pro Asp Val Pro Arg Leu Gly Ser Thr	
625 630 635 640	

ttc agt ctg gat acc tcc atg agt atg aat agc agc cca tta gta ggt Phe Ser Leu Asp Thr Ser Met Ser Met Asn Ser Ser Pro Leu Val Gly 645 650 655	1968
cca gag tgt gac cac ccc aaa atc aaa cct tcc tca tct gcc aat gcc Pro Glu Cys Asp His Pro Lys Ile Lys Pro Ser Ser Ser Ala Asn Ala 660 665 670	2016
att tat tct ctg gct gcc aga cct ctt cct gtg cca aaa ctg cca cct Ile Tyr Ser Leu Ala Ala Arg Pro Leu Pro Val Pro Lys Leu Pro Pro 675 680 685	2064
ggg gag caa tgt gag ggt gaa gag gac aca gag ttc atg act ccc tct Gly Glu Gln Cys Glu Gly Glu Glu Asp Thr Glu Phe Met Thr Pro Ser 690 695 700	2112
tcc agg cct cta cgg cct ttg gat aca tcc cag agt tca cga gca tgt Ser Arg Pro Leu Arg Pro Leu Asp Thr Ser Gln Ser Ser Arg Ala Cys 705 710 715 720	2160
gat tgc gac cag cag att gat agc tgt acg tat gaa gca atg tat aat Asp Cys Asp Gln Gln Ile Asp Ser Cys Thr Tyr Glu Ala Met Tyr Asn 725 730 735	2208
att cag tcc cag gcg cca tct atc acc gag agc agc acc ttt ggt gaa Ile Gln Ser Gln Ala Pro Ser Ile Thr Glu Ser Ser Thr Phe Gly Glu 740 745 750	2256
ggg aat ttg gcc gca gcc cat gcc aac act ggt ccc gag gag tca gaa Gly Asn Leu Ala Ala Ala His Ala Asn Thr Gly Pro Glu Glu Ser Glu 755 760 765	2304
aat gag gat gat ggg tat gat gtc cca aag cca cct gtg ccg gcc gtg Asn Glu Asp Asp Gly Tyr Asp Val Pro Lys Pro Pro Val Pro Ala Val 770 775 780	2352
ctg gcc cgc cga act ctc tca gat atc tct aat gcc agc tcc tcc ttt Leu Ala Arg Arg Thr Leu Ser Asp Ile Ser Asn Ala Ser Ser Ser Phe 785 790 795 800	2400
ggc tgg ttg tct ctg gat ggt gat cct aca aca aat gtc act gaa ggt Gly Trp Leu Ser Leu Asp Gly Asp Pro Thr Thr Asn Val Thr Glu Gly 805 810 815	2448
tcc caa gtt ccc gag agg cct cca aaa cca ttc ccg cgg aga atc aac Ser Gln Val Pro Glu Arg Pro Pro Lys Pro Phe Pro Arg Arg Ile Asn 820 825 830	2496
tct gaa cgg aaa gct ggc agc tgt cag caa ggt agt ggt cct gcc gcc Ser Glu Arg Lys Ala Gly Ser Cys Gln Gln Gly Ser Gly Pro Ala Ala 835 840 845	2544
tct gct gcc acc gcc tca cct cag ctc tcc agt gag atc gag aac ctc Ser Ala Ala Thr Ala Ser Pro Gln Leu Ser Ser Glu Ile Glu Asn Leu 850 855 860	2592
atg agt cag ggg tac tcc tac cag gac atc cag aaa gct ttg gtc att Met Ser Gln Gly Tyr Ser Tyr Gln Asp Ile Gln Lys Ala Leu Val Ile 865 870 875 880	2640
gcc cag aac aac atc gag atg gcc aaa aac atc ctc cgg gaa ttt gtt	2688

Ala Gln Asn Asn Ile Glu Met Ala Lys Asn Ile Leu Arg Glu Phe Val
 885 890 895

tcc att tct tct cct gcc cat gta gct acc tag
 Ser Ile Ser Ser Pro Ala His Val Ala Thr
 900 905

2721

<210> 252

<211> 906

<212> .PRT

<213> c-Cbl Y700F

<400> 252

Met Ala Gly Asn Val Lys Lys Ser Ser Gly Ala Gly Gly Gly Thr Gly
 1 5 10 15

Ser Gly Gly Ser Gly Ser Gly Gly Leu Ile Gly Leu Met Lys Asp Ala
 20 25 30

Phe Gln Pro His His His His His His His Leu Ser Pro His Pro Pro
 35 40 45

Gly Thr Val Asp Lys Lys Met Val Glu Lys Cys Trp Lys Leu Met Asp
 50 55 60

Lys Val Val Arg Leu Cys Gln Asn Pro Lys Leu Ala Leu Lys Asn Ser
 65 70 75 80

Pro Pro Tyr Ile Leu Asp Leu Leu Pro Asp Thr Tyr Gln His Leu Arg
 85 90 95

Thr Ile Leu Ser Arg Tyr Glu Gly Lys Met Glu Thr Leu Gly Glu Asn
 100 105 110

Glu Tyr Phe Arg Val Phe Met Glu Asn Leu Met Lys Lys Thr Lys Gln
 115 120 125

Thr Ile Ser Leu Phe Lys Glu Gly Lys Glu Arg Met Tyr Glu Glu Asn
 130 135 140

Ser Gln Pro Arg Arg Asn Leu Thr Lys Leu Ser Leu Ile Phe Ser His
 145 150 155 160

Met Leu Ala Glu Leu Lys Gly Ile Phe Pro Ser Gly Leu Phe Gln Gly
 165 170 175

Asp Thr Phe Arg Ile Thr Lys Ala Asp Ala Ala Glu Phe Trp Arg Lys
 180 185 190

Ala Phe Gly Glu Lys Thr Ile Val Pro Trp Lys Ser Phe Arg Gln Ala
 195 200 205

Leu His Glu Val His Pro Ile Ser Ser Gly Leu Glu Ala Met Ala Leu
 210 215 220

Lys Ser Thr Ile Asp Leu Thr Cys Asn Asp Tyr Ile Ser Val Phe Glu
 225 230 235 240
 Phe Asp Ile Phe Thr Arg Leu Phe Gln Pro Trp Ser Ser Leu Leu Arg
 245 250 255
 Asn Trp Asn Ser Leu Ala Val Thr His Pro Gly Tyr Met Ala Phe Leu
 260 265 270
 Thr Tyr Asp Glu Val Lys Ala Arg Leu Gln Lys Phe Ile His Lys Pro
 275 280 285
 Gly Ser Tyr Ile Phe Arg Leu Ser Cys Thr Arg Leu Gly Gln Trp Ala
 290 295 300
 Ile Gly Tyr Val Thr Ala Asp Gly Asn Ile Leu Gln Thr Ile Pro His
 305 310 315 320
 Asn Lys Pro Leu Phe Gln Ala Leu Ile Asp Gly Phe Arg Glu Gly Phe
 325 330 335
 Tyr Leu Phe Pro Asp Gly Arg Asn Gln Asn Pro Asp Leu Thr Gly Leu
 340 345 350
 Cys Glu Pro Thr Pro Gln Asp His Ile Lys Val Thr Gln Glu Gln Tyr
 355 360 365
 Glu Leu Tyr Cys Glu Met Gly Ser Thr Phe Gln Leu Cys Lys Ile Cys
 370 375 380
 Ala Glu Asn Asp Lys Asp Val Lys Ile Glu Pro Cys Gly His Leu Met
 385 390 395 400
 Cys Thr Ser Cys Leu Thr Ser Trp Gln Glu Ser Glu Gly Gln Gly Cys
 405 410 415
 Pro Phe Cys Arg Cys Glu Ile Lys Gly Thr Glu Pro Ile Val Val Asp
 420 425 430
 Pro Phe Asp Pro Arg Gly Ser Gly Ser Leu Leu Arg Gln Gly Ala Glu
 435 440 445
 Gly Ala Pro Ser Pro Asn Tyr Asp Asp Asp Asp Glu Arg Ala Asp
 450 455 460
 Asp Thr Leu Phe Met Met Lys Glu Leu Ala Gly Ala Lys Val Glu Arg
 465 470 475 480
 Pro Pro Ser Pro Phe Ser Met Ala Pro Gln Ala Ser Leu Pro Pro Val
 485 490 495
 Pro Pro Arg Leu Asp Leu Leu Pro Gln Arg Val Cys Val Pro Ser Ser
 500 505 510
 Ala Ser Ala Leu Gly Thr Ala Ser Lys Ala Ala Ser Gly Ser Leu His
 515 520 525
 Lys Asp Lys Pro Leu Pro Val Pro Pro Thr Leu Arg Asp Leu Pro Pro
 530 535 540
 Pro Pro Pro Pro Asp Arg Pro Tyr Ser Val Gly Ala Glu Ser Arg Pro

545		550		555		560
Gln Arg Arg Pro	Leu Pro Cys Thr Pro	Gly Asp Cys Pro Ser	Arg Asp			
	565	570	575			
Lys Leu Pro Pro	Val Pro Ser Ser Arg	Leu Gly Asp Ser	Trp Leu Pro			
	580	585	590			
Arg Pro Ile Pro	Lys Val Pro Val Ser	Ala Pro Ser Ser	Ser Asp Pro			
	595	600	605			
Trp Thr Gly Arg	Glu Leu Thr Asn Arg	His Ser Leu Pro	Phe Ser Leu			
	610	615	620			
Pro Ser Gln Met	Glu Pro Arg Pro Asp	Val Pro Arg Leu	Gly Ser Thr			
	625	630	635			640
Phe Ser Leu Asp	Thr Ser Met Ser Met	Asn Ser Ser Pro	Leu Val Gly			
	645	650	655			
Pro Glu Cys Asp	His Pro Lys Ile Lys	Pro Ser Ser Ser	Ala Asn Ala			
	660	665	670			
Ile Tyr Ser Leu	Ala Ala Arg Pro Leu	Pro Val Pro Lys	Leu Pro Pro			
	675	680	685			
Gly Glu Gln Cys	Glu Gly Glu Glu Asp	Thr Glu Phe Met	Thr Pro Ser			
	690	695	700			
Ser Arg Pro Leu	Arg Pro Leu Asp Thr	Ser Gln Ser Ser	Arg Ala Cys			
	705	710	715			720
Asp Cys Asp Gln	Gln Ile Asp Ser Cys	Thr Tyr Glu Ala	Met Tyr Asn			
	725	730	735			
Ile Gln Ser Gln	Ala Pro Ser Ile Thr	Glu Ser Ser Thr	Phe Gly Glu			
	740	745	750			
Gly Asn Leu Ala	Ala Ala His Ala Asn	Thr Gly Pro Glu	Glu Ser Glu			
	755	760	765			
Asn Glu Asp Asp	Gly Tyr Asp Val Pro	Lys Pro Pro Val	Pro Ala Val			
	770	775	780			
Leu Ala Arg Arg	Thr Leu Ser Asp Ile	Ser Asn Ala Ser	Ser Ser Phe			
	785	790	795			800
Gly Trp Leu Ser	Leu Asp Gly Asp Pro	Thr Thr Asn Val	Thr Glu Gly			
	805	810	815			
Ser Gln Val Pro	Glu Arg Pro Pro Lys	Pro Phe Pro Arg	Arg Ile Asn			
	820	825	830			
Ser Glu Arg Lys	Ala Gly Ser Cys Gln	Gln Gly Ser Gly	Pro Ala Ala			
	835	840	845			
Ser Ala Ala Thr	Ala Ser Pro Gln Leu	Ser Ser Glu Ile	Glu Asn Leu			
	850	855	860			
Met Ser Gln Gly	Tyr Ser Tyr Gln Asp	Ile Gln Lys Ala	Leu Val Ile			
	865	870	875			880

Ala Gln Asn Asn Ile Glu Met Ala Lys Asn Ile Leu Arg Glu Phe Val
 885 890 895

Ser Ile Ser Ser Pro Ala His Val Ala Thr
 900 905

<210> 253

<211> 2721

<212> DNA

<213> c-Cbl Y731F

<220>

<221> CDS

<222> (1) .. (2718)

<223>

<400> 253

atg gcc ggc aac gtg aag aag agc tct ggg gcc ggg ggc ggc acg ggc	48
Met Ala Gly Asn Val Lys Lys Ser Ser Gly Ala Gly Gly Gly Thr Gly	
1 5 10 15	
tcc ggg ggc tcg ggt tcg ggt ggc ctg att ggg ctc atg aag gac gcc	96
Ser Gly Gly Ser Gly Ser Gly Gly Leu Ile Gly Leu Met Lys Asp Ala	
20 25 30	
ttc cag ccg cac cac cac cac cac cac ctc agc ccc cac ccg ccg	144
Phe Gln Pro His His His His His His His Leu Ser Pro His Pro Pro	
35 40 45	
ggg acg gtg gac aag aag atg gtg gag aag tgc tgg aag ctc atg gac	192
Gly Thr Val Asp Lys Lys Met Val Glu Lys Cys Trp Lys Leu Met Asp	
50 55 60	
aag gtg gtg cgg ttg tgt cag aac cca aag ctg gcg cta aag aat agc	240
Lys Val Val Arg Leu Cys Gln Asn Pro Lys Leu Ala Leu Lys Asn Ser	
65 70 75 80	
cca cct tat atc tta gac ctg cta cca gat acc tac cag cat ctc cgt	288
Pro Pro Tyr Ile Leu Asp Leu Leu Pro Asp Thr Tyr Gln His Leu Arg	
85 90 95	
act atc ttg tca aga tat gag ggg aag atg gag aca ctt gga gaa aat	336
Thr Ile Leu Ser Arg Tyr Glu Gly Lys Met Glu Thr Leu Gly Glu Asn	
100 105 110	
gag tat ttt agg gtg ttt atg gag aat ttg atg aag aaa act aag caa	384
Glu Tyr Phe Arg Val Phe Met Glu Asn Leu Met Lys Lys Thr Lys Gln	
115 120 125	
acc ata agc ctc ttc aag gag gga aaa gaa aga atg tat gag gag aat	432

Thr 130	Ile	Ser	Leu	Phe	Lys	Glu 135	Gly	Lys	Glu	Arg 140	Met	Tyr	Glu	Glu	Asn	
tct	cag	cct	agg	cga	aac	cta	acc	aaa	ctg	tcc	ctc	atc	ttc	agc	cac	480
Ser 145	Gln	Pro	Arg	Arg	Asn 150	Leu	Thr	Lys	Leu	Ser 155	Leu	Ile	Phe	Ser	His 160	
atg	ctg	gca	gaa	cta	aaa	gga	atc	ttt	cca	agt	gga	ctc	ttt	cag	gga	528
Met 165	Leu	Ala	Glu	Leu 165	Lys	Gly	Ile	Phe	Pro 170	Ser	Gly	Leu	Phe	Gln 175	Gly	
gac	aca	ttt	cgg	att	act	aaa	gca	gat	gct	gcg	gaa	ttt	tggt	aga	aaa	576
Asp 180	Thr	Phe	Arg	Ile	Thr	Lys	Ala	Asp 185	Ala	Ala	Glu	Phe	Trp 190	Arg	Lys	
gct	ttt	ggg	gaa	aag	aca	ata	gtc	cct	tggt	aag	agc	ttt	cga	cag	gct	624
Ala 195	Phe	Gly	Glu	Lys	Thr	Ile	Val 200	Pro	Trp	Lys	Ser	Phe 205	Arg	Gln	Ala	
cta	cat	gaa	gtg	cat	ccc	atc	agt	tct	ggg	ctg	gag	gcc	atg	gct	ctg	672
Leu 210	His	Glu	Val	His	Pro	Ile	Ser	Ser	Gly	Leu	Glu	Ala	Met	Ala	Leu	
aaa	tcc	act	att	gat	ctg	acc	tgc	aat	gat	tat	att	tgc	gtt	ttt	gaa	720
Lys 225	Ser	Thr	Ile	Asp	Leu	Thr	Cys	Asn	Asp	Tyr 235	Ile	Ser	Val	Phe	Glu 240	
ttt	gac	atc	ttt	acc	cga	ctc	ttt	cag	ccc	tggt	tcc	tct	ttg	ctc	agg	768
Phe 245	Asp	Ile	Phe	Thr	Arg	Leu	Phe	Gln	Pro 250	Trp	Ser	Ser	Leu	Leu 255	Arg	
aat	tggt	aac	agc	ctt	gct	gta	act	cat	cct	ggc	tac	atg	gct	ttt	ttg	816
Asn 260	Trp	Asn	Ser	Leu	Ala	Val	Thr	His 265	Pro	Gly	Tyr	Met	Ala	Phe	Leu	
acg	tat	gac	gaa	gtg	aaa	gct	cgg	ctc	cag	aaa	ttc	att	cac	aaa	cct	864
Thr 275	Tyr	Asp	Glu	Val	Lys	Ala	Arg	Leu	Gln	Lys	Phe	Ile 285	His	Lys	Pro	
ggc	agt	tat	atc	ttc	cgg	ctg	agc	tgt	act	cgt	ctg	ggt	cag	tggt	gct	912
Gly 290	Ser	Tyr	Ile	Phe	Arg	Leu	Ser	Cys	Thr	Arg	Leu	Gly	Gln	Trp	Ala	
att	ggg	tat	gtt	act	gct	gat	ggg	aac	att	ctc	cag	aca	atc	cct	cac	960
Ile 305	Gly	Tyr	Val	Thr	Ala	Asp	Gly	Asn	Ile	Leu 315	Gln	Thr	Ile	Pro	His 320	
aat	aaa	cct	ctc	ttc	caa	gca	ctg	att	gat	ggc	ttc	agg	gaa	ggc	ttc	1008
Asn 325	Lys	Pro	Leu	Phe	Gln	Ala	Leu	Ile	Asp 330	Gly	Phe	Arg	Glu	Gly	Phe 335	
tat	ttg	ttt	cct	gat	gga	cga	aat	cag	aat	cct	gat	ctg	act	ggc	tta	1056
Tyr 340	Leu	Phe	Pro	Asp	Gly	Arg	Asn	Gln	Asn 345	Pro	Asp	Leu	Thr	Gly	Leu	
tgt	gaa	cca	act	ccc	caa	gac	cat	atc	aaa	gtg	acc	cag	gaa	caa	tat	1104
Cys 355	Glu	Pro	Thr	Pro	Gln	Asp	His	Ile	Lys	Val	Thr	Gln	Glu	Gln	Tyr	
gaa	tta	tac	tgt	gag	atg	ggc	tcc	aca	ttc	caa	cta	tgt	aaa	ata	tgt	1152
Glu	Leu	Tyr	Cys	Glu	Met	Gly	Ser	Thr	Phe	Gln	Leu	Cys	Lys	Ile	Cys	

370	375	380	
gct gaa aat gat aag gat gta aag att gag ccc tgt gga cac ctc atg			1200
Ala Glu Asn Asp Lys Asp Val Lys Ile Glu Pro Cys Gly His Leu Met			
385	390	395	400
tgc aca tcc tgt ctt aca tcc tgg cag gaa tca gaa ggt cag ggc tgt			1248
Cys Thr Ser Cys Leu Thr Ser Trp Gln Glu Ser Glu Gly Gln Gly Cys			
	405	410	415
cct ttc tgc cga tgt gaa att aaa ggt act gaa ccc atc gtg gta gat			1296
Pro Phe Cys Arg Cys Glu Ile Lys Gly Thr Glu Pro Ile Val Val Asp			
	420	425	430
ccg ttt gat cct aga ggg agt ggc agc ctg ttg agg caa gga gca gag			1344
Pro Phe Asp Pro Arg Gly Ser Gly Ser Leu Leu Arg Gln Gly Ala Glu			
	435	440	445
gga gct ccc tcc cca aat tat gat gat gat gat gat gaa cga gct gat			1392
Gly Ala Pro Ser Pro Asn Tyr Asp Asp Asp Asp Asp Glu Arg Ala Asp			
	450	455	460
gat act ctc ttc atg atg aag gaa ttg gct ggt gcc aag gtg gaa cgg			1440
Asp Thr Leu Phe Met Met Lys Glu Leu Ala Gly Ala Lys Val Glu Arg			
465	470	475	480
ccg cct tct cca ttc tcc atg gcc cca caa gct tcc ctt ccc ccg gtg			1488
Pro Pro Ser Pro Phe Ser Met Ala Pro Gln Ala Ser Leu Pro Pro Val			
	485	490	495
cca cca cga ctt gac ctt ctg ccg cag cga gta tgt gtt ccc tca agt			1536
Pro Pro Arg Leu Asp Leu Leu Pro Gln Arg Val Cys Val Pro Ser Ser			
	500	505	510
gct tct gct ctt gga act gct tct aag gct gct tct ggc tcc ctt cat			1584
Ala Ser Ala Leu Gly Thr Ala Ser Lys Ala Ala Ser Gly Ser Leu His			
	515	520	525
aaa gac aaa cca ttg cca gta cct ccc aca ctt cga gat ctt cca cca			1632
Lys Asp Lys Pro Leu Pro Val Pro Pro Thr Leu Arg Asp Leu Pro Pro			
	530	535	540
cca ccg cct cca gac cgg cca tat tct gtt gga gca gaa tcc cga cct			1680
Pro Pro Pro Pro Asp Arg Pro Tyr Ser Val Gly Ala Glu Ser Arg Pro			
545	550	555	560
caa aga cgc ccc ttg cct tgt aca cca ggc gac tgt ccc tcc aga gac			1728
Gln Arg Arg Pro Leu Pro Cys Thr Pro Gly Asp Cys Pro Ser Arg Asp			
	565	570	575
aaa ctg ccc cct gtc ccc tct agc cgc ctt gga gac tca tgg ctg ccc			1776
Lys Leu Pro Pro Val Pro Ser Ser Arg Leu Gly Asp Ser Trp Leu Pro			
	580	585	590
cgg cca atc ccc aaa gta cca gta tct gcc cca agt tcc agt gat ccc			1824
Arg Pro Ile Pro Lys Val Pro Val Ser Ala Pro Ser Ser Ser Asp Pro			
	595	600	605
tgg aca gga aga gaa tta acc aac cgg cac tca ctt cca ttt tca ttg			1872
Trp Thr Gly Arg Glu Leu Thr Asn Arg His Ser Leu Pro Phe Ser Leu			
	610	615	620

ccc tca caa atg gag ccc aga cca gat gtg cct agg ctc gga agc acg	1920
Pro Ser Gln Met Glu Pro Arg Pro Asp Val Pro Arg Leu Gly Ser Thr	
625 630 635 640	
ttc agt ctg gat acc tcc atg agt atg aat agc agc cca tta gta ggt	1968
Phe Ser Leu Asp Thr Ser Met Ser Met Asn Ser Ser Pro Leu Val Gly	
645 650 655	
cca gag tgt gac cac ccc aaa atc aaa cct tcc tca tct gcc aat gcc	2016
Pro Glu Cys Asp His Pro Lys Ile Lys Pro Ser Ser Ser Ala Asn Ala	
660 665 670	
att tat tct ctg gct gcc aga cct ctt cct gtg cca aaa ctg cca cct	2064
Ile Tyr Ser Leu Ala Ala Arg Pro Leu Pro Val Pro Lys Leu Pro Pro	
675 680 685	
ggg gag caa tgt gag ggt gaa gag gac aca gag tac atg act ccc tct	2112
Gly Glu Gln Cys Glu Gly Glu Glu Asp Thr Glu Tyr Met Thr Pro Ser	
690 695 700	
tcc agg cct cta cgg cct ttg gat aca tcc cag agt tca cga gca tgt	2160
Ser Arg Pro Leu Arg Pro Leu Asp Thr Ser Gln Ser Ser Arg Ala Cys	
705 710 715 720	
gat tgc gac cag cag att gat agc tgt acg ttt gaa gca atg tat aat	2208
Asp Cys Asp Gln Gln Ile Asp Ser Cys Thr Phe Glu Ala Met Tyr Asn	
725 730 735	
att cag tcc cag gcg cca tct atc acc gag agc agc acc ttt ggt gaa	2256
Ile Gln Ser Gln Ala Pro Ser Ile Thr Glu Ser Ser Thr Phe Gly Glu	
740 745 750	
ggg aat ttg gcc gca gcc cat gcc aac act ggt ccc gag gag tca gaa	2304
Gly Asn Leu Ala Ala His Ala Asn Thr Gly Pro Glu Glu Ser Glu	
755 760 765	
aat gag gat gat ggg tat gat gtc cca aag cca cct gtg ccg gcc gtg	2352
Asn Glu Asp Asp Gly Tyr Asp Val Pro Lys Pro Pro Val Pro Ala Val	
770 775 780	
ctg gcc cgc cga act ctc tca gat atc tct aat gcc agc tcc tcc ttt	2400
Leu Ala Arg Arg Thr Leu Ser Asp Ile Ser Asn Ala Ser Ser Ser Phe	
785 790 795 800	
ggc tgg ttg tct ctg gat ggt gat cct aca aca aat gtc act gaa ggt	2448
Gly Trp Leu Ser Leu Asp Gly Asp Pro Thr Thr Asn Val Thr Glu Gly	
805 810 815	
tcc caa gtt ccc gag agg cct cca aaa cca ttc ccg cgg aga atc aac	2496
Ser Gln Val Pro Glu Arg Pro Pro Lys Pro Phe Pro Arg Arg Ile Asn	
820 825 830	
tct gaa cgg aaa gct ggc agc tgt cag caa ggt agt ggt cct gcc gcc	2544
Ser Glu Arg Lys Ala Gly Ser Cys Gln Gln Gly Ser Gly Pro Ala Ala	
835 840 845	
tct gct gcc acc gcc tca cct cag ctc tcc agt gag atc gag aac ctc	2592
Ser Ala Ala Thr Ala Ser Pro Gln Leu Ser Ser Glu Ile Glu Asn Leu	
850 855 860	

65/88

atg agt cag ggg tac tcc tac cag gac atc cag aaa gct ttg gtc att 2640
 Met Ser Gln Gly Tyr Ser Tyr Gln Asp Ile Gln Lys Ala Leu Val Ile
 865 870 875 880

gcc cag aac aac atc gag atg gcc aaa aac atc ctc cgg gaa ttt gtt 2688
 Ala Gln Asn Asn Ile Glu Met Ala Lys Asn Ile Leu Arg Glu Phe Val
 885 890 895

tcc att tct tct cct gcc cat gta gct acc tag 2721
 Ser Ile Ser Ser Pro Ala His Val Ala Thr
 900 905

<210> 254

<211> 906

<212> PRT

<213> c-Cbl Y731F

<400> 254

Met Ala Gly Asn Val Lys Lys Ser Ser Gly Ala Gly Gly Gly Thr Gly
 1 5 10 15

Ser Gly Gly Ser Gly Ser Gly Gly Leu Ile Gly Leu Met Lys Asp Ala
 20 25 30

Phe Gln Pro His His His His His His His Leu Ser Pro His Pro Pro
 35 40 45

Gly Thr Val Asp Lys Lys Met Val Glu Lys Cys Trp Lys Leu Met Asp
 50 55 60

Lys Val Val Arg Leu Cys Gln Asn Pro Lys Leu Ala Leu Lys Asn Ser
 65 70 75 80

Pro Pro Tyr Ile Leu Asp Leu Leu Pro Asp Thr Tyr Gln His Leu Arg
 85 90 95

Thr Ile Leu Ser Arg Tyr Glu Gly Lys Met Glu Thr Leu Gly Glu Asn
 100 105 110

Glu Tyr Phe Arg Val Phe Met Glu Asn Leu Met Lys Lys Thr Lys Gln
 115 120 125

Thr Ile Ser Leu Phe Lys Glu Gly Lys Glu Arg Met Tyr Glu Glu Asn
 130 135 140

Ser Gln Pro Arg Arg Asn Leu Thr Lys Leu Ser Leu Ile Phe Ser His
 145 150 155 160

Met Leu Ala Glu Leu Lys Gly Ile Phe Pro Ser Gly Leu Phe Gln Gly
 165 170 175

Asp Thr Phe Arg Ile Thr Lys Ala Asp Ala Ala Glu Phe Trp Arg Lys
 180 185 190

Ala Phe Gly Glu Lys Thr Ile Val Pro Trp Lys Ser Phe Arg Gln Ala
 195 200 205
 Leu His Glu Val His Pro Ile Ser Ser Gly Leu Glu Ala Met Ala Leu
 210 215 220
 Lys Ser Thr Ile Asp Leu Thr Cys Asn Asp Tyr Ile Ser Val Phe Glu
 225 230 235 240
 Phe Asp Ile Phe Thr Arg Leu Phe Gln Pro Trp Ser Ser Leu Leu Arg
 245 250 255
 Asn Trp Asn Ser Leu Ala Val Thr His Pro Gly Tyr Met Ala Phe Leu
 260 265 270
 Thr Tyr Asp Glu Val Lys Ala Arg Leu Gln Lys Phe Ile His Lys Pro
 275 280 285
 Gly Ser Tyr Ile Phe Arg Leu Ser Cys Thr Arg Leu Gly Gln Trp Ala
 290 295 300
 Ile Gly Tyr Val Thr Ala Asp Gly Asn Ile Leu Gln Thr Ile Pro His
 305 310 315 320
 Asn Lys Pro Leu Phe Gln Ala Leu Ile Asp Gly Phe Arg Glu Gly Phe
 325 330 335
 Tyr Leu Phe Pro Asp Gly Arg Asn Gln Asn Pro Asp Leu Thr Gly Leu
 340 345 350
 Cys Glu Pro Thr Pro Gln Asp His Ile Lys Val Thr Gln Glu Gln Tyr
 355 360 365
 Glu Leu Tyr Cys Glu Met Gly Ser Thr Phe Gln Leu Cys Lys Ile Cys
 370 375 380
 Ala Glu Asn Asp Lys Asp Val Lys Ile Glu Pro Cys Gly His Leu Met
 385 390 395 400
 Cys Thr Ser Cys Leu Thr Ser Trp Gln Glu Ser Glu Gly Gln Gly Cys
 405 410 415
 Pro Phe Cys Arg Cys Glu Ile Lys Gly Thr Glu Pro Ile Val Val Asp
 420 425 430
 Pro Phe Asp Pro Arg Gly Ser Gly Ser Leu Leu Arg Gln Gly Ala Glu
 435 440 445
 Gly Ala Pro Ser Pro Asn Tyr Asp Asp Asp Asp Asp Glu Arg Ala Asp
 450 455 460
 Asp Thr Leu Phe Met Met Lys Glu Leu Ala Gly Ala Lys Val Glu Arg
 465 470 475 480
 Pro Pro Ser Pro Phe Ser Met Ala Pro Gln Ala Ser Leu Pro Pro Val
 485 490 495
 Pro Pro Arg Leu Asp Leu Leu Pro Gln Arg Val Cys Val Pro Ser Ser
 500 505 510

Ala Ser Ala Leu Gly Thr Ala Ser Lys Ala Ala Ser Gly Ser Leu His
 515 520 525
 Lys Asp Lys Pro Leu Pro Val Pro Pro Thr Leu Arg Asp Leu Pro Pro
 530 535 540
 Pro Pro Pro Pro Asp Arg Pro Tyr Ser Val Gly Ala Glu Ser Arg Pro
 545 550 555 560
 Gln Arg Arg Pro Leu Pro Cys Thr Pro Gly Asp Cys Pro Ser Arg Asp
 565 570 575
 Lys Leu Pro Pro Val Pro Ser Ser Arg Leu Gly Asp Ser Trp Leu Pro
 580 585 590
 Arg Pro Ile Pro Lys Val Pro Val Ser Ala Pro Ser Ser Ser Asp Pro
 595 600 605
 Trp Thr Gly Arg Glu Leu Thr Asn Arg His Ser Leu Pro Phe Ser Leu
 610 615 620
 Pro Ser Gln Met Glu Pro Arg Pro Asp Val Pro Arg Leu Gly Ser Thr
 625 630 635 640
 Phe Ser Leu Asp Thr Ser Met Ser Met Asn Ser Ser Pro Leu Val Gly
 645 650 655
 Pro Glu Cys Asp His Pro Lys Ile Lys Pro Ser Ser Ser Ala Asn Ala
 660 665 670
 Ile Tyr Ser Leu Ala Ala Arg Pro Leu Pro Val Pro Lys Leu Pro Pro
 675 680 685
 Gly Glu Gln Cys Glu Gly Glu Glu Asp Thr Glu Tyr Met Thr Pro Ser
 690 695 700
 Ser Arg Pro Leu Arg Pro Leu Asp Thr Ser Gln Ser Ser Arg Ala Cys
 705 710 715 720
 Asp Cys Asp Gln Gln Ile Asp Ser Cys Thr Phe Glu Ala Met Tyr Asn
 725 730 735
 Ile Gln Ser Gln Ala Pro Ser Ile Thr Glu Ser Ser Thr Phe Gly Glu
 740 745 750
 Gly Asn Leu Ala Ala Ala His Ala Asn Thr Gly Pro Glu Glu Ser Glu
 755 760 765
 Asn Glu Asp Asp Gly Tyr Asp Val Pro Lys Pro Pro Val Pro Ala Val
 770 775 780
 Leu Ala Arg Arg Thr Leu Ser Asp Ile Ser Asn Ala Ser Ser Ser Phe
 785 790 795 800
 Gly Trp Leu Ser Leu Asp Gly Asp Pro Thr Thr Asn Val Thr Glu Gly
 805 810 815
 Ser Gln Val Pro Glu Arg Pro Pro Lys Pro Phe Pro Arg Arg Ile Asn
 820 825 830

Ser Glu Arg Lys Ala Gly Ser Cys Gln Gln Gly Ser Gly Pro Ala Ala
835 840 845

Ser Ala Ala Thr Ala Ser Pro Gln Leu Ser Ser Glu Ile Glu Asn Leu
850 855 860

Met Ser Gln Gly Tyr Ser Tyr Gln Asp Ile Gln Lys Ala Leu Val Ile
865 870 875 880

Ala Gln Asn Asn Ile Glu Met Ala Lys Asn Ile Leu Arg Glu Phe Val
885 890 895

Ser Ile Ser Ser Pro Ala His Val Ala Thr
900 905

<210> 255

<211> 2721

<212> DNA

<213> c-Cbl Y774F

<220>

<221> CDS

<222> (1) .. (2718)

<223>

<400> 255

atg gcc ggc aac gtg aag aag agc tct ggg gcc ggg ggc ggc acg ggc	48
Met Ala Gly Asn Val Lys Lys Ser Ser Gly Ala Gly Gly Gly Thr Gly	
1 5 10 15	
tcc ggg ggc tcc ggt tcc ggt ggc ctg att ggg ctc atg aag gac gcc	96
Ser Gly Gly Ser Gly Ser Gly Gly Leu Ile Gly Leu Met Lys Asp Ala	
20 25 30	
ttc cag ccg cac cac cac cac cac cac ctc agc ccc cac ccg ccg	144
Phe Gln Pro His His His His His His His Leu Ser Pro His Pro Pro	
35 40 45	
ggg acg gtg gac aag aag atg gtg gag aag tgc tgg aag ctc atg gac	192
Gly Thr Val Asp Lys Lys Met Val Glu Lys Cys Trp Lys Leu Met Asp	
50 55 60	
aag gtg gtg cgg ttg tgt cag aac cca aag ctg gcg cta aag aat agc	240
Lys Val Val Arg Leu Cys Gln Asn Pro Lys Leu Ala Leu Lys Asn Ser	
65 70 75 80	
cca cct tat atc tta gac ctg cta cca gat acc tac cag cat ctc cgt	288
Pro Pro Tyr Ile Leu Asp Leu Leu Pro Asp Thr Tyr Gln His Leu Arg	
85 90 95	

act atc ttg tca aga tat gag ggg aag atg gag aca ctt gga gaa aat	336
Thr Ile Leu Ser Arg Tyr Glu Gly Lys Met Glu Thr Leu Gly Glu Asn	
100 105 110	
gag tat ttt agg gtg ttt atg gag aat ttg atg aag aaa act aag caa	384
Glu Tyr Phe Arg Val Phe Met Glu Asn Leu Met Lys Lys Thr Lys Gln	
115 120 125	
acc ata agc ctc ttc aag gag gga aaa gaa aga atg tat gag gag aat	432
Thr Ile Ser Leu Phe Lys Glu Gly Lys Glu Arg Met Tyr Glu Glu Asn	
130 135 140	
tct cag cct agg cga aac cta acc aaa ctg tcc ctc atc ttc agc cac	480
Ser Gln Pro Arg Arg Asn Leu Thr Lys Leu Ser Leu Ile Phe Ser His	
145 150 155 160	
atg ctg gca gaa cta aaa gga atc ttt cca agt gga ctc ttt cag gga	528
Met Leu Ala Glu Leu Lys Gly Ile Phe Pro Ser Gly Leu Phe Gln Gly	
165 170 175	
gac aca ttt cgg att act aaa gca gat gct gcg gaa ttt tgg aga aaa	576
Asp Thr Phe Arg Ile Thr Lys Ala Asp Ala Ala Glu Phe Trp Arg Lys	
180 185 190	
gct ttt ggg gaa aag aca ata gtc cct tgg aag agc ttt cga cag gct	624
Ala Phe Gly Glu Lys Thr Ile Val Pro Trp Lys Ser Phe Arg Gln Ala	
195 200 205	
cta cat gaa gtg cat ccc atc agt tct ggg ctg gag gcc atg gct ctg	672
Leu His Glu Val His Pro Ile Ser Ser Gly Leu Glu Ala Met Ala Leu	
210 215 220	
aaa tcc act att gat ctg acc tgc aat gat tat att tcg gtt ttt gaa	720
Lys Ser Thr Ile Asp Leu Thr Cys Asn Asp Tyr Ile Ser Val Phe Glu	
225 230 235 240	
ttt gac atc ttt acc cga ctc ttt cag ccc tgg tcc tct ttg ctc agg	768
Phe Asp Ile Phe Thr Arg Leu Phe Gln Pro Trp Ser Ser Leu Leu Arg	
245 250 255	
aat tgg aac agc ctt gct gta act cat cct ggc tac atg gct ttt ttg	816
Asn Trp Asn Ser Leu Ala Val Thr His Pro Gly Tyr Met Ala Phe Leu	
260 265 270	
acg tat gac gaa gtg aaa gct cgg ctc cag aaa ttc att cac aaa cct	864
Thr Tyr Asp Glu Val Lys Ala Arg Leu Gln Lys Phe Ile His Lys Pro	
275 280 285	
ggc agt tat atc ttc cgg ctg agc tgt act cgt ctg ggt cag tgg gct	912
Gly Ser Tyr Ile Phe Arg Leu Ser Cys Thr Arg Leu Gly Gln Trp Ala	
290 295 300	
att ggg tat gtt act gct gat ggg aac att ctc cag aca atc cct cac	960
Ile Gly Tyr Val Thr Ala Asp Gly Asn Ile Leu Gln Thr Ile Pro His	
305 310 315 320	
aat aaa cct ctc ttc caa gca ctg att gat ggc ttc agg gaa ggc ttc	1008
Asn Lys Pro Leu Phe Gln Ala Leu Ile Asp Gly Phe Arg Glu Gly Phe	
325 330 335	
tat ttg ttt cct gat gga cga aat cag aat cct gat ctg act ggc tta	1056

Tyr	Leu	Phe	Pro	Asp	Gly	Arg	Asn	Gln	Asn	Pro	Asp	Leu	Thr	Gly	Leu		
			340					345					350				
tgt	gaa	cca	act	ccc	caa	gac	cat	atc	aaa	gtg	acc	cag	gaa	caa	tat	1104	
Cys	Glu	Pro	Thr	Pro	Gln	Asp	His	Ile	Lys	Val	Thr	Gln	Glu	Gln	Tyr		
		355					360					365					
gaa	tta	tac	tgt	gag	atg	ggc	tcc	aca	ttc	caa	cta	tgt	aaa	ata	tgt	1152	
Glu	Leu	Tyr	Cys	Glu	Met	Gly	Ser	Thr	Phe	Gln	Leu	Cys	Lys	Ile	Cys		
	370					375					380						
gct	gaa	aat	gat	aag	gat	gta	aag	att	gag	ccc	tgt	gga	cac	ctc	atg	1200	
Ala	Glu	Asn	Asp	Lys	Asp	Val	Lys	Ile	Glu	Pro	Cys	Gly	His	Leu	Met		
385					390					395					400		
tgc	aca	tcc	tgt	ctt	aca	tcc	tgg	cag	gaa	tca	gaa	ggg	cag	ggc	tgt	1248	
Cys	Thr	Ser	Cys	Leu	Thr	Ser	Trp	Gln	Glu	Ser	Glu	Gly	Gln	Gly	Cys		
			405					410					415				
cct	ttc	tgc	cga	tgt	gaa	att	aaa	ggg	act	gaa	ccc	atc	gtg	gta	gat	1296	
Pro	Phe	Cys	Arg	Cys	Glu	Ile	Lys	Gly	Thr	Glu	Pro	Ile	Val	Val	Asp		
			420					425					430				
ccg	ttt	gat	cct	aga	ggg	agt	ggc	agc	ctg	ttg	agg	caa	gga	gca	gag	1344	
Pro	Phe	Asp	Pro	Arg	Gly	Ser	Gly	Ser	Leu	Leu	Arg	Gln	Gly	Ala	Glu		
		435					440					445					
gga	gct	ccc	tcc	cca	aat	tat	gat	gat	gat	gat	gat	gaa	cga	gct	gat	1392	
Gly	Ala	Pro	Ser	Pro	Asn	Tyr	Asp	Asp	Asp	Asp	Asp	Glu	Arg	Ala	Asp		
	450					455						460					
gat	act	ctc	ttc	atg	atg	aag	gaa	ttg	gct	ggg	gcc	aag	gtg	gaa	cgg	1440	
Asp	Thr	Leu	Phe	Met	Met	Lys	Glu	Leu	Ala	Gly	Ala	Lys	Val	Glu	Arg		
465					470				475						480		
ccg	cct	tct	cca	ttc	tcc	atg	gcc	cca	caa	gct	tcc	ctt	ccc	ccg	gtg	1488	
Pro	Pro	Ser	Pro	Phe	Ser	Met	Ala	Pro	Gln	Ala	Ser	Leu	Pro	Pro	Val		
			485					490					495				
cca	cca	cga	ctt	gac	ctt	ctg	ccg	cag	cga	gta	tgt	gtt	ccc	tca	agt	1536	
Pro	Pro	Arg	Leu	Asp	Leu	Leu	Pro	Gln	Arg	Val	Cys	Val	Pro	Ser	Ser		
			500					505					510				
gct	tct	gct	ctt	gga	act	gct	tct	aag	gct	gct	tct	ggc	tcc	ctt	cat	1584	
Ala	Ser	Ala	Leu	Gly	Thr	Ala	Ser	Lys	Ala	Ala	Ser	Gly	Ser	Leu	His		
		515					520					525					
aaa	gac	aaa	cca	ttg	cca	gta	cct	ccc	aca	ctt	cga	gat	ctt	cca	cca	1632	
Lys	Asp	Lys	Pro	Leu	Pro	Val	Pro	Pro	Thr	Leu	Arg	Asp	Leu	Pro	Pro		
	530					535					540						
cca	ccg	cct	cca	gac	cgg	cca	tat	tct	gtt	gga	gca	gaa	tcc	cga	cct	1680	
Pro	Pro	Pro	Pro	Asp	Arg	Pro	Tyr	Ser	Val	Gly	Ala	Glu	Ser	Arg	Pro		
545					550					555					560		
caa	aga	cgc	ccc	ttg	cct	tgt	aca	cca	ggc	gac	tgt	ccc	tcc	aga	gac	1728	
Gln	Arg	Arg	Pro	Leu	Pro	Cys	Thr	Pro	Gly	Asp	Cys	Pro	Ser	Arg	Asp		
			565						570				575				
aaa	ctg	ccc	cct	gtc	ccc	tct	agc	cgc	ctt	gga	gac	tca	tgg	ctg	ccc	1776	
Lys	Leu	Pro	Pro	Val	Pro	Ser	Ser	Arg	Leu	Gly	Asp	Ser	Trp	Leu	Pro		

580	585	590	
cgg cca atc ccc aaa gta cca gta tct gcc cca agt tcc agt gat ccc Arg Pro Ile Pro Lys Val Pro Val Ser Ala Pro Ser Ser Ser Asp Pro 595 600 605			1824
tgg aca gga aga gaa tta acc aac cgg cac tca ctt cca ttt tca ttg Trp Thr Gly Arg Glu Leu Thr Asn Arg His Ser Leu Pro Phe Ser Leu 610 615 620			1872
ccc tca caa atg gag ccc aga cca gat gtg cct agg ctc gga agc acg Pro Ser Gln Met Glu Pro Arg Pro Asp Val Pro Arg Leu Gly Ser Thr 625 630 635 640			1920
ttc agt ctg gat acc tcc atg agt atg aat agc agc cca tta gta ggt Phe Ser Leu Asp Thr Ser Met Ser Met Asn Ser Ser Pro Leu Val Gly 645 650 655			1968
cca gag tgt gac cac ccc aaa atc aaa cct tcc tca tct gcc aat gcc Pro Glu Cys Asp His Pro Lys Ile Lys Pro Ser Ser Ser Ala Asn Ala 660 665 670			2016
att tat tct ctg gct gcc aga cct ctt cct gtg cca aaa ctg cca cct Ile Tyr Ser Leu Ala Ala Arg Pro Leu Pro Val Pro Lys Leu Pro Pro 675 680 685			2064
ggg gag caa tgt gag ggt gaa gag gac aca gag tac atg act ccc tct Gly Glu Gln Cys Glu Gly Glu Glu Asp Thr Glu Tyr Met Thr Pro Ser 690 695 700			2112
tcc agg cct cta cgg cct ttg gat aca tcc cag agt tca cga gca tgt Ser Arg Pro Leu Arg Pro Leu Asp Thr Ser Gln Ser Ser Arg Ala Cys 705 710 715 720			2160
gat tgc gac cag cag att gat agc tgt acg tat gaa gca atg tat aat Asp Cys Asp Gln Gln Ile Asp Ser Cys Thr Tyr Glu Ala Met Tyr Asn 725 730 735			2208
att cag tcc cag gcg cca tct atc acc gag agc agc acc ttt ggt gaa Ile Gln Ser Gln Ala Pro Ser Ile Thr Glu Ser Ser Thr Phe Gly Glu 740 745 750			2256
ggg aat ttg gcc gca gcc cat gcc aac act ggt ccc gag gag tca gaa Gly Asn Leu Ala Ala Ala His Ala Asn Thr Gly Pro Glu Glu Ser Glu 755 760 765			2304
aat gag gat gat ggg ttt gat gtc cca aag cca cct gtg ccg gcc gtg Asn Glu Asp Asp Gly Phe Asp Val Pro Lys Pro Pro Val Pro Ala Val 770 775 780			2352
ctg gcc cgc cga act ctc tca gat atc tct aat gcc agc tcc tcc ttt Leu Ala Arg Arg Thr Leu Ser Asp Ile Ser Asn Ala Ser Ser Ser Phe 785 790 795 800			2400
ggc tgg ttg tct ctg gat ggt gat cct aca aca aat gtc act gaa ggt Gly Trp Leu Ser Leu Asp Gly Asp Pro Thr Thr Asn Val Thr Glu Gly 805 810 815			2448
tcc caa gtt ccc gag agg cct cca aaa cca ttc ccg cgg aga atc aac Ser Gln Val Pro Glu Arg Pro Pro Lys Pro Phe Pro Arg Arg Ile Asn 820 825 830			2496

tct gaa cgg aaa gct ggc agc tgt cag caa ggt agt ggt cct gcc gcc 2544
 Ser Glu Arg Lys Ala Gly Ser Cys Gln Gln Gly Ser Gly Pro Ala Ala
 835 840 845

tct gct gcc acc gcc tca cct cag ctc tcc agt gag atc gag aac ctc 2592
 Ser Ala Ala Thr Ala Ser Pro Gln Leu Ser Ser Glu Ile Glu Asn Leu
 850 855 860

atg agt cag ggg tac tcc tac cag gac atc cag aaa gct ttg gtc att 2640
 Met Ser Gln Gly Tyr Ser Tyr Gln Asp Ile Gln Lys Ala Leu Val Ile
 865 870 875 880

gcc cag aac aac atc gag atg gcc aaa aac atc ctc cgg gaa ttt gtt 2688
 Ala Gln Asn Asn Ile Glu Met Ala Lys Asn Ile Leu Arg Glu Phe Val
 885 890 895

tcc att tct tct cct gcc cat gta gct acc tag 2721
 Ser Ile Ser Ser Pro Ala His Val Ala Thr
 900 905

<210> 256

<211> 906

<212> PRT

<213> c-Cbl Y774F

<400> 256

Met Ala Gly Asn Val Lys Lys Ser Ser Gly Ala Gly Gly Gly Thr Gly
 1 5 10 15

Ser Gly Gly Ser Gly Ser Gly Gly Leu Ile Gly Leu Met Lys Asp Ala
 20 25 30

Phe Gln Pro His His His His His His His Leu Ser Pro His Pro Pro
 35 40 45

Gly Thr Val Asp Lys Lys Met Val Glu Lys Cys Trp Lys Leu Met Asp
 50 55 60

Lys Val Val Arg Leu Cys Gln Asn Pro Lys Leu Ala Leu Lys Asn Ser
 65 70 75 80

Pro Pro Tyr Ile Leu Asp Leu Leu Pro Asp Thr Tyr Gln His Leu Arg
 85 90 95

Thr Ile Leu Ser Arg Tyr Glu Gly Lys Met Glu Thr Leu Gly Glu Asn
 100 105 110

Glu Tyr Phe Arg Val Phe Met Glu Asn Leu Met Lys Lys Thr Lys Gln
 115 120 125

Thr Ile Ser Leu Phe Lys Glu Gly Lys Glu Arg Met Tyr Glu Glu Asn
 130 135 140

Ser Gln Pro Arg Arg Asn Leu Thr Lys Leu Ser Leu Ile Phe Ser His

145	150	155	160
Met Leu Ala Glu Leu Lys Gly Ile Phe Pro Ser Gly Leu Phe Gln Gly	165	170	175
Asp Thr Phe Arg Ile Thr Lys Ala Asp Ala Ala Glu Phe Trp Arg Lys	180	185	190
Ala Phe Gly Glu Lys Thr Ile Val Pro Trp Lys Ser Phe Arg Gln Ala	195	200	205
Leu His Glu Val His Pro Ile Ser Ser Gly Leu Glu Ala Met Ala Leu	210	215	220
Lys Ser Thr Ile Asp Leu Thr Cys Asn Asp Tyr Ile Ser Val Phe Glu	225	230	235
Phe Asp Ile Phe Thr Arg Leu Phe Gln Pro Trp Ser Ser Leu Leu Arg	245	250	255
Asn Trp Asn Ser Leu Ala Val Thr His Pro Gly Tyr Met Ala Phe Leu	260	265	270
Thr Tyr Asp Glu Val Lys Ala Arg Leu Gln Lys Phe Ile His Lys Pro	275	280	285
Gly Ser Tyr Ile Phe Arg Leu Ser Cys Thr Arg Leu Gly Gln Trp Ala	290	295	300
Ile Gly Tyr Val Thr Ala Asp Gly Asn Ile Leu Gln Thr Ile Pro His	305	310	315
Asn Lys Pro Leu Phe Gln Ala Leu Ile Asp Gly Phe Arg Glu Gly Phe	325	330	335
Tyr Leu Phe Pro Asp Gly Arg Asn Gln Asn Pro Asp Leu Thr Gly Leu	340	345	350
Cys Glu Pro Thr Pro Gln Asp His Ile Lys Val Thr Gln Glu Gln Tyr	355	360	365
Glu Leu Tyr Cys Glu Met Gly Ser Thr Phe Gln Leu Cys Lys Ile Cys	370	375	380
Ala Glu Asn Asp Lys Asp Val Lys Ile Glu Pro Cys Gly His Leu Met	385	390	395
Cys Thr Ser Cys Leu Thr Ser Trp Gln Glu Ser Glu Gly Gln Gly Cys	405	410	415
Pro Phe Cys Arg Cys Glu Ile Lys Gly Thr Glu Pro Ile Val Val Asp	420	425	430
Pro Phe Asp Pro Arg Gly Ser Gly Ser Leu Leu Arg Gln Gly Ala Glu	435	440	445
Gly Ala Pro Ser Pro Asn Tyr Asp Asp Asp Asp Asp Glu Arg Ala Asp	450	455	460
Asp Thr Leu Phe Met Met Lys Glu Leu Ala Gly Ala Lys Val Glu Arg	465	470	475
			480

Pro Pro Ser Pro Phe Ser Met Ala Pro Gln Ala Ser Leu Pro Pro Val
 485 490 495
 Pro Pro Arg Leu Asp Leu Leu Pro Gln Arg Val Cys Val Pro Ser Ser
 500 505 510
 Ala Ser Ala Leu Gly Thr Ala Ser Lys Ala Ala Ser Gly Ser Leu His
 515 520 525
 Lys Asp Lys Pro Leu Pro Val Pro Pro Thr Leu Arg Asp Leu Pro Pro
 530 535 540
 Pro Pro Pro Pro Asp Arg Pro Tyr Ser Val Gly Ala Glu Ser Arg Pro
 545 550 555 560
 Gln Arg Arg Pro Leu Pro Cys Thr Pro Gly Asp Cys Pro Ser Arg Asp
 565 570 575
 Lys Leu Pro Pro Val Pro Ser Ser Arg Leu Gly Asp Ser Trp Leu Pro
 580 585 590
 Arg Pro Ile Pro Lys Val Pro Val Ser Ala Pro Ser Ser Ser Asp Pro
 595 600 605
 Trp Thr Gly Arg Glu Leu Thr Asn Arg His Ser Leu Pro Phe Ser Leu
 610 615 620
 Pro Ser Gln Met Glu Pro Arg Pro Asp Val Pro Arg Leu Gly Ser Thr
 625 630 635 640
 Phe Ser Leu Asp Thr Ser Met Ser Met Asn Ser Ser Pro Leu Val Gly
 645 650 655
 Pro Glu Cys Asp His Pro Lys Ile Lys Pro Ser Ser Ser Ala Asn Ala
 660 665 670
 Ile Tyr Ser Leu Ala Ala Arg Pro Leu Pro Val Pro Lys Leu Pro Pro
 675 680 685
 Gly Glu Gln Cys Glu Gly Glu Glu Asp Thr Glu Tyr Met Thr Pro Ser
 690 695 700
 Ser Arg Pro Leu Arg Pro Leu Asp Thr Ser Gln Ser Ser Arg Ala Cys
 705 710 715 720
 Asp Cys Asp Gln Gln Ile Asp Ser Cys Thr Tyr Glu Ala Met Tyr Asn
 725 730 735
 Ile Gln Ser Gln Ala Pro Ser Ile Thr Glu Ser Ser Thr Phe Gly Glu
 740 745 750
 Gly Asn Leu Ala Ala Ala His Ala Asn Thr Gly Pro Glu Glu Ser Glu
 755 760 765
 Asn Glu Asp Asp Gly Phe Asp Val Pro Lys Pro Pro Val Pro Ala Val
 770 775 780
 Leu Ala Arg Arg Thr Leu Ser Asp Ile Ser Asn Ala Ser Ser Ser Phe
 785 790 795 800

Gly Trp Leu Ser Leu Asp Gly Asp Pro Thr Thr Asn Val Thr Glu Gly
 805 810 815

Ser Gln Val Pro Glu Arg Pro Pro Lys Pro Phe Pro Arg Arg Ile Asn
 820 825 830

Ser Glu Arg Lys Ala Gly Ser Cys Gln Gln Gly Ser Gly Pro Ala Ala
 835 840 845

Ser Ala Ala Thr Ala Ser Pro Gln Leu Ser Ser Glu Ile Glu Asn Leu
 850 855 860

Met Ser Gln Gly Tyr Ser Tyr Gln Asp Ile Gln Lys Ala Leu Val Ile
 865 870 875 880

Ala Gln Asn Asn Ile Glu Met Ala Lys Asn Ile Leu Arg Glu Phe Val
 885 890 895

Ser Ile Ser Ser Pro Ala His Val Ala Thr
 900 905

<210> 257

<211> 2721

<212> DNA

<213> c-Cbl Y700F/Y731F/Y774F

<220>

<221> CDS

<222> (1) .. (2718)

<223>

<400> 257

atg gcc ggc aac gtg aag aag agc tct ggg gcc ggg ggc ggc acg ggc 48
 Met Ala Gly Asn Val Lys Lys Ser Ser Gly Ala Gly Gly Gly Thr Gly
 1 5 10 15

tcc ggg ggc tcg ggt tcg ggt ggc ctg att ggg ctc atg aag gac gcc 96
 Ser Gly Gly Ser Gly Ser Gly Gly Leu Ile Gly Leu Met Lys Asp Ala
 20 25 30

ttc cag ccg cac cac cac cac cac cac ctc agc ccc cac ccg ccg 144
 Phe Gln Pro His His His His His His His Leu Ser Pro His Pro Pro
 35 40 45

ggg acg gtg gac aag aag atg gtg gag aag tgc tgg aag ctc atg gac 192
 Gly Thr Val Asp Lys Lys Met Val Glu Lys Cys Trp Lys Leu Met Asp
 50 55 60

aag gtg gtg cgg ttg tgt cag aac cca aag ctg gcg cta aag aat agc 240
 Lys Val Val Arg Leu Cys Gln Asn Pro Lys Leu Ala Leu Lys Asn Ser
 65 70 75 80

cca cct tat atc tta gac ctg cta cca gat acc tac cag cat ctc cgt	288
Pro Pro Tyr Ile Leu Asp Leu Leu Pro Asp Thr Tyr Gln His Leu Arg	
85 90 95	
act atc ttg tca aga tat gag ggg aag atg gag aca ctt gga gaa aat	336
Thr Ile Leu Ser Arg Tyr Glu Gly Lys Met Glu Thr Leu Gly Glu Asn	
100 105 110	
gag tat ttt agg gtg ttt atg gag aat ttg atg aag aaa act aag caa	384
Glu Tyr Phe Arg Val Phe Met Glu Asn Leu Met Lys Lys Thr Lys Gln	
115 120 125	
acc ata agc ctc ttc aag gag gga aaa gaa aga atg tat gag gag aat	432
Thr Ile Ser Leu Phe Lys Glu Gly Lys Glu Arg Met Tyr Glu Glu Asn	
130 135 140	
tct cag cct agg cga aac cta acc aaa ctg tcc ctc atc ttc agc cac	480
Ser Gln Pro Arg Arg Asn Leu Thr Lys Leu Ser Leu Ile Phe Ser His	
145 150 155 160	
atg ctg gca gaa cta aaa gga atc ttt cca agt gga ctc ttt cag gga	528
Met Leu Ala Glu Leu Lys Gly Ile Phe Pro Ser Gly Leu Phe Gln Gly	
165 170 175	
gac aca ttt cgg att act aaa gca gat gct gcg gaa ttt tgg aga aaa	576
Asp Thr Phe Arg Ile Thr Lys Ala Asp Ala Ala Glu Phe Trp Arg Lys	
180 185 190	
gct ttt ggg gaa aag aca ata gtc cct tgg aag agc ttt cga cag gct	624
Ala Phe Gly Glu Lys Thr Ile Val Pro Trp Lys Ser Phe Arg Gln Ala	
195 200 205	
cta cat gaa gtg cat ccc atc agt tct ggg ctg gag gcc atg gct ctg	672
Leu His Glu Val His Pro Ile Ser Ser Gly Leu Glu Ala Met Ala Leu	
210 215 220	
aaa tcc act att gat ctg acc tgc aat gat tat att tgc gtt ttt gaa	720
Lys Ser Thr Ile Asp Leu Thr Cys Asn Asp Tyr Ile Ser Val Phe Glu	
225 230 235 240	
ttt gac atc ttt acc cga ctc ttt cag ccc tgg tcc tct ttg ctc agg	768
Phe Asp Ile Phe Thr Arg Leu Phe Gln Pro Trp Ser Ser Leu Leu Arg	
245 250 255	
aat tgg aac agc ctt gct gta act cat cct ggc tac atg gct ttt ttg	816
Asn Trp Asn Ser Leu Ala Val Thr His Pro Gly Tyr Met Ala Phe Leu	
260 265 270	
acg tat gac gaa gtg aaa gct cgg ctc cag aaa ttc att cac aaa cct	864
Thr Tyr Asp Glu Val Lys Ala Arg Leu Gln Lys Phe Ile His Lys Pro	
275 280 285	
ggc agt tat atc ttc cgg ctg agc tgt act cgt ctg ggt cag tgg gct	912
Gly Ser Tyr Ile Phe Arg Leu Ser Cys Thr Arg Leu Gly Gln Trp Ala	
290 295 300	
att ggg tat gtt act gct gat ggg aac att ctc cag aca atc cct cac	960
Ile Gly Tyr Val Thr Ala Asp Gly Asn Ile Leu Gln Thr Ile Pro His	
305 310 315 320	

aat aaa cct ctc ttc caa gca ctg att gat ggc ttc agg gaa ggc ttc	1008
Asn Lys Pro Leu Phe Gln Ala Leu Ile Asp Gly Phe Arg Glu Gly Phe	
325 330 335	
tat ttg ttt cct gat gga cga aat cag aat cct gat ctg act ggc tta	1056
Tyr Leu Phe Pro Asp Gly Arg Asn Gln Asn Pro Asp Leu Thr Gly Leu	
340 345 350	
tgt gaa cca act ccc caa gac cat atc aaa gtg acc cag gaa caa tat	1104
Cys Glu Pro Thr Pro Gln Asp His Ile Lys Val Thr Gln Glu Gln Tyr	
355 360 365	
gaa tta tac tgt gag atg ggc tcc aca ttc caa cta tgt aaa ata tgt	1152
Glu Leu Tyr Cys Glu Met Gly Ser Thr Phe Gln Leu Cys Lys Ile Cys	
370 375 380	
gct gaa aat gat aag gat gta aag att gag ccc tgt gga cac ctc atg	1200
Ala Glu Asn Asp Lys Asp Val Lys Ile Glu Pro Cys Gly His Leu Met	
385 390 395 400	
tgc aca tcc tgt ctt aca tcc tgg cag gaa tca gaa ggt cag ggc tgt	1248
Cys Thr Ser Cys Leu Thr Ser Trp Gln Glu Ser Glu Gly Gln Gly Cys	
405 410 415	
cct ttc tgc cga tgt gaa att aaa ggt act gaa ccc atc gtg gta gat	1296
Pro Phe Cys Arg Cys Glu Ile Lys Gly Thr Glu Pro Ile Val Val Asp	
420 425 430	
ccg ttt gat cct aga ggg agt ggc agc ctg ttg agg caa gga gca gag	1344
Pro Phe Asp Pro Arg Gly Ser Gly Ser Leu Leu Arg Gln Gly Ala Glu	
435 440 445	
gga gct ccc tcc cca aat tat gat gat gat gat gat gaa cga gct gat	1392
Gly Ala Pro Ser Pro Asn Tyr Asp Asp Asp Asp Asp Glu Arg Ala Asp	
450 455 460	
gat act ctc ttc atg atg aag gaa ttg gct ggt gcc aag gtg gaa cgg	1440
Asp Thr Leu Phe Met Met Lys Glu Leu Ala Gly Ala Lys Val Glu Arg	
465 470 475 480	
ccg cct tct cca ttc tcc atg gcc cca caa gct tcc ctt ccc ccg gtg	1488
Pro Pro Ser Pro Phe Ser Met Ala Pro Gln Ala Ser Leu Pro Pro Val	
485 490 495	
cca cca cga ctt gac ctt ctg ccg cag cga gta tgt gtt ccc tca agt	1536
Pro Pro Arg Leu Asp Leu Leu Pro Gln Arg Val Cys Val Pro Ser Ser	
500 505 510	
gct tct gct ctt gga act gct tct aag gct gct tct ggc tcc ctt cat	1584
Ala Ser Ala Leu Gly Thr Ala Ser Lys Ala Ala Ser Gly Ser Leu His	
515 520 525	
aaa gac aaa cca ttg cca gta cct ccc aca ctt cga gat ctt cca cca	1632
Lys Asp Lys Pro Leu Pro Val Pro Pro Thr Leu Arg Asp Leu Pro Pro	
530 535 540	
cca ccg cct cca gac cgg cca tat tct gtt gga gca gaa tcc cga cct	1680
Pro Pro Pro Pro Asp Arg Pro Tyr Ser Val Gly Ala Glu Ser Arg Pro	
545 550 555 560	
caa aga cgc ccc ttg cct tgt aca cca ggc gac tgt ccc tcc aga gac	1728

Gln	Arg	Arg	Pro	Leu	Pro	Cys	Thr	Pro	Gly	Asp	Cys	Pro	Ser	Arg	Asp	
			565						570					575		
aaa	ctg	ccc	cct	gtc	ccc	tct	agc	cgc	ctt	gga	gac	tca	tgg	ctg	ccc	1776
Lys	Leu	Pro	Pro	Val	Pro	Ser	Ser	Arg	Leu	Gly	Asp	Ser	Trp	Leu	Pro	
			580					585					590			
cgg	cca	atc	ccc	aaa	gta	cca	gta	tct	gcc	cca	agt	tcc	agt	gat	ccc	1824
Arg	Pro	Ile	Pro	Lys	Val	Pro	Val	Ser	Ala	Pro	Ser	Ser	Ser	Asp	Pro	
			595				600					605				
tgg	aca	gga	aga	gaa	tta	acc	aac	cgg	cac	tca	ctt	cca	ttt	tca	ttg	1872
Trp	Thr	Gly	Arg	Glu	Leu	Thr	Asn	Arg	His	Ser	Leu	Pro	Phe	Ser	Leu	
	610					615					620					
ccc	tca	caa	atg	gag	ccc	aga	cca	gat	gtg	cct	agg	ctc	gga	agc	acg	1920
Pro	Ser	Gln	Met	Glu	Pro	Arg	Pro	Asp	Val	Pro	Arg	Leu	Gly	Ser	Thr	
625					630					635					640	
ttc	agt	ctg	gat	acc	tcc	atg	agt	atg	aat	agc	agc	cca	tta	gta	ggc	1968
Phe	Ser	Leu	Asp	Thr	Ser	Met	Ser	Met	Asn	Ser	Ser	Pro	Leu	Val	Gly	
				645					650					655		
cca	gag	tgt	gac	cac	ccc	aaa	atc	aaa	cct	tcc	tca	tct	gcc	aat	gcc	2016
Pro	Glu	Cys	Asp	His	Pro	Lys	Ile	Lys	Pro	Ser	Ser	Ser	Ala	Asn	Ala	
			660					665					670			
att	tat	tct	ctg	gct	gcc	aga	cct	ctt	cct	gtg	cca	aaa	ctg	cca	cct	2064
Ile	Tyr	Ser	Leu	Ala	Ala	Arg	Pro	Leu	Pro	Val	Pro	Lys	Leu	Pro	Pro	
			675				680					685				
ggg	gag	caa	tgt	gag	ggc	gaa	gag	gac	aca	gag	ttc	atg	act	ccc	tct	2112
Gly	Glu	Gln	Cys	Glu	Gly	Glu	Glu	Asp	Thr	Glu	Phe	Met	Thr	Pro	Ser	
	690					695					700					
tcc	agg	cct	cta	cgg	cct	ttg	gat	aca	tcc	cag	agt	tca	cga	gca	tgt	2160
Ser	Arg	Pro	Leu	Arg	Pro	Leu	Asp	Thr	Ser	Gln	Ser	Ser	Arg	Ala	Cys	
705					710					715					720	
gat	tgc	gac	cag	cag	att	gat	agc	tgt	acg	ttt	gaa	gca	atg	tat	aat	2208
Asp	Cys	Asp	Gln	Gln	Ile	Asp	Ser	Cys	Thr	Phe	Glu	Ala	Met	Tyr	Asn	
				725				730						735		
att	cag	tcc	cag	gcg	cca	tct	atc	acc	gag	agc	agc	acc	ttt	ggc	gaa	2256
Ile	Gln	Ser	Gln	Ala	Pro	Ser	Ile	Thr	Glu	Ser	Ser	Thr	Phe	Gly	Glu	
			740					745					750			
ggg	aat	ttg	gcc	gca	gcc	cat	gcc	aac	act	ggc	ccc	gag	gag	tca	gaa	2304
Gly	Asn	Leu	Ala	Ala	Ala	His	Ala	Asn	Thr	Gly	Pro	Glu	Glu	Ser	Glu	
		755					760					765				
aat	gag	gat	gat	ggg	ttt	gat	gtc	cca	aag	cca	cct	gtg	ccg	gcc	gtg	2352
Asn	Glu	Asp	Asp	Gly	Phe	Asp	Val	Pro	Lys	Pro	Pro	Val	Pro	Ala	Val	
	770					775						780				
ctg	gcc	cgc	cga	act	ctc	tca	gat	atc	tct	aat	gcc	agc	tcc	tcc	ttt	2400
Leu	Ala	Arg	Arg	Thr	Leu	Ser	Asp	Ile	Ser	Asn	Ala	Ser	Ser	Ser	Phe	
785					790					795					800	
ggc	tgg	ttg	tct	ctg	gat	ggc	gat	cct	aca	aca	aat	gtc	act	gaa	ggc	2448
Gly	Trp	Leu	Ser	Leu	Asp	Gly	Asp	Pro	Thr	Thr	Asn	Val	Thr	Glu	Gly	

79/88

805	810	815	
tcc caa gtt ccc gag agg cct cca aaa cca ttc ccg cgg aga atc aac Ser Gln Val Pro Glu Arg Pro Pro Lys Pro Phe Pro Arg Arg Ile Asn 820 825 830			2496
tct gaa cgg aaa gct ggc agc tgt cag caa ggt agt ggt cct gcc gcc Ser Glu Arg Lys Ala Gly Ser Cys Gln Gln Gly Ser Gly Pro Ala Ala 835 840 845			2544
tct gct gcc acc gcc tca cct cag ctc tcc agt gag atc gag aac ctc Ser Ala Ala Thr Ala Ser Pro Gln Leu Ser Ser Glu Ile Glu Asn Leu 850 855 860			2592
atg agt cag ggg tac tcc tac cag gac atc cag aaa gct ttg gtc att Met Ser Gln Gly Tyr Ser Tyr Gln Asp Ile Gln Lys Ala Leu Val Ile 865 870 875 880			2640
gcc cag aac aac atc gag atg gcc aaa aac atc ctc cgg gaa ttt gtt Ala Gln Asn Asn Ile Glu Met Ala Lys Asn Ile Leu Arg Glu Phe Val 885 890 895			2688
tcc att tct tct cct gcc cat gta gct acc tag Ser Ile Ser Ser Pro Ala His Val Ala Thr 900 905			2721
<210> 258			
<211> 906			
<212> PRT			
<213> c-Cbl Y700F/Y731F/Y774F			
<400> 258			
Met Ala Gly Asn Val Lys Lys Ser Ser Gly Ala Gly Gly Gly Thr Gly 1 5 10 15			
Ser Gly Gly Ser Gly Ser Gly Gly Leu Ile Gly Leu Met Lys Asp Ala 20 25 30			
Phe Gln Pro His His His His His His His Leu Ser Pro His Pro Pro 35 40 45			
Gly Thr Val Asp Lys Lys Met Val Glu Lys Cys Trp Lys Leu Met Asp 50 55 60			
Lys Val Val Arg Leu Cys Gln Asn Pro Lys Leu Ala Leu Lys Asn Ser 65 70 75 80			
Pro Pro Tyr Ile Leu Asp Leu Leu Pro Asp Thr Tyr Gln His Leu Arg 85 90 95			
Thr Ile Leu Ser Arg Tyr Glu Gly Lys Met Glu Thr Leu Gly Glu Asn 100 105 110			
Glu Tyr Phe Arg Val Phe Met Glu Asn Leu Met Lys Lys Thr Lys Gln 115 120 125			

Thr Ile Ser Leu Phe Lys Glu Gly Lys Glu Arg Met Tyr Glu Glu Asn
 130 135 140
 Ser Gln Pro Arg Arg Asn Leu Thr Lys Leu Ser Leu Ile Phe Ser His
 145 150 155 160
 Met Leu Ala Glu Leu Lys Gly Ile Phe Pro Ser Gly Leu Phe Gln Gly
 165 170 175
 Asp Thr Phe Arg Ile Thr Lys Ala Asp Ala Ala Glu Phe Trp Arg Lys
 180 185 190
 Ala Phe Gly Glu Lys Thr Ile Val Pro Trp Lys Ser Phe Arg Gln Ala
 195 200 205
 Leu His Glu Val His Pro Ile Ser Ser Gly Leu Glu Ala Met Ala Leu
 210 215 220
 Lys Ser Thr Ile Asp Leu Thr Cys Asn Asp Tyr Ile Ser Val Phe Glu
 225 230 235 240
 Phe Asp Ile Phe Thr Arg Leu Phe Gln Pro Trp Ser Ser Leu Leu Arg
 245 250 255
 Asn Trp Asn Ser Leu Ala Val Thr His Pro Gly Tyr Met Ala Phe Leu
 260 265 270
 Thr Tyr Asp Glu Val Lys Ala Arg Leu Gln Lys Phe Ile His Lys Pro
 275 280 285
 Gly Ser Tyr Ile Phe Arg Leu Ser Cys Thr Arg Leu Gly Gln Trp Ala
 290 295 300
 Ile Gly Tyr Val Thr Ala Asp Gly Asn Ile Leu Gln Thr Ile Pro His
 305 310 315 320
 Asn Lys Pro Leu Phe Gln Ala Leu Ile Asp Gly Phe Arg Glu Gly Phe
 325 330 335
 Tyr Leu Phe Pro Asp Gly Arg Asn Gln Asn Pro Asp Leu Thr Gly Leu
 340 345 350
 Cys Glu Pro Thr Pro Gln Asp His Ile Lys Val Thr Gln Glu Gln Tyr
 355 360 365
 Glu Leu Tyr Cys Glu Met Gly Ser Thr Phe Gln Leu Cys Lys Ile Cys
 370 375 380
 Ala Glu Asn Asp Lys Asp Val Lys Ile Glu Pro Cys Gly His Leu Met
 385 390 395 400
 Cys Thr Ser Cys Leu Thr Ser Trp Gln Glu Ser Glu Gly Gln Gly Cys
 405 410 415
 Pro Phe Cys Arg Cys Glu Ile Lys Gly Thr Glu Pro Ile Val Val Asp
 420 425 430
 Pro Phe Asp Pro Arg Gly Ser Gly Ser Leu Leu Arg Gln Gly Ala Glu

Gly	Ala	Pro	Ser	Pro	Asn	Tyr	Asp	Asp	Asp	Asp	Asp	Glu	Arg	Ala	Asp
450						455						460			
Asp	Thr	Leu	Phe	Met	Met	Lys	Glu	Leu	Ala	Gly	Ala	Lys	Val	Glu	Arg
465					470					475					480
Pro	Pro	Ser	Pro	Phe	Ser	Met	Ala	Pro	Gln	Ala	Ser	Leu	Pro	Pro	Val
				485					490					495	
Pro	Pro	Arg	Leu	Asp	Leu	Leu	Pro	Gln	Arg	Val	Cys	Val	Pro	Ser	Ser
			500					505					510		
Ala	Ser	Ala	Leu	Gly	Thr	Ala	Ser	Lys	Ala	Ala	Ser	Gly	Ser	Leu	His
		515					520					525			
Lys	Asp	Lys	Pro	Leu	Pro	Val	Pro	Pro	Thr	Leu	Arg	Asp	Leu	Pro	Pro
	530					535						540			
Pro	Pro	Pro	Pro	Asp	Arg	Pro	Tyr	Ser	Val	Gly	Ala	Glu	Ser	Arg	Pro
545					550					555					560
Gln	Arg	Arg	Pro	Leu	Pro	Cys	Thr	Pro	Gly	Asp	Cys	Pro	Ser	Arg	Asp
				565					570					575	
Lys	Leu	Pro	Pro	Val	Pro	Ser	Ser	Arg	Leu	Gly	Asp	Ser	Trp	Leu	Pro
			580					585					590		
Arg	Pro	Ile	Pro	Lys	Val	Pro	Val	Ser	Ala	Pro	Ser	Ser	Ser	Asp	Pro
		595					600					605			
Trp	Thr	Gly	Arg	Glu	Leu	Thr	Asn	Arg	His	Ser	Leu	Pro	Phe	Ser	Leu
	610					615					620				
Pro	Ser	Gln	Met	Glu	Pro	Arg	Pro	Asp	Val	Pro	Arg	Leu	Gly	Ser	Thr
625					630					635					640
Phe	Ser	Leu	Asp	Thr	Ser	Met	Ser	Met	Asn	Ser	Ser	Pro	Leu	Val	Gly
				645					650					655	
Pro	Glu	Cys	Asp	His	Pro	Lys	Ile	Lys	Pro	Ser	Ser	Ser	Ala	Asn	Ala
			660					665					670		
Ile	Tyr	Ser	Leu	Ala	Ala	Arg	Pro	Leu	Pro	Val	Pro	Lys	Leu	Pro	Pro
		675					680					685			
Gly	Glu	Gln	Cys	Glu	Gly	Glu	Glu	Asp	Thr	Glu	Phe	Met	Thr	Pro	Ser
	690					695					700				
Ser	Arg	Pro	Leu	Arg	Pro	Leu	Asp	Thr	Ser	Gln	Ser	Ser	Arg	Ala	Cys
705					710					715					720
Asp	Cys	Asp	Gln	Gln	Ile	Asp	Ser	Cys	Thr	Phe	Glu	Ala	Met	Tyr	Asn
				725					730					735	
Ile	Gln	Ser	Gln	Ala	Pro	Ser	Ile	Thr	Glu	Ser	Ser	Thr	Phe	Gly	Glu
			740					745					750		

Gly Asn Leu Ala Ala Ala His Ala Asn Thr Gly Pro Glu Glu Ser Glu
755 760 765

Asn Glu Asp Asp Gly Phe Asp Val Pro Lys Pro Pro Val Pro Ala Val
770 775 780

Leu Ala Arg Arg Thr Leu Ser Asp Ile Ser Asn Ala Ser Ser Ser Phe
785 790 795 800

Gly Trp Leu Ser Leu Asp Gly Asp Pro Thr Thr Asn Val Thr Glu Gly
805 810 815

Ser Gln Val Pro Glu Arg Pro Pro Lys Pro Phe Pro Arg Arg Ile Asn
820 825 830

Ser Glu Arg Lys Ala Gly Ser Cys Gln Gln Gly Ser Gly Pro Ala Ala
835 840 845

Ser Ala Ala Thr Ala Ser Pro Gln Leu Ser Ser Glu Ile Glu Asn Leu
850 855 860

Met Ser Gln Gly Tyr Ser Tyr Gln Asp Ile Gln Lys Ala Leu Val Ile
865 870 875 880

Ala Gln Asn Asn Ile Glu Met Ala Lys Asn Ile Leu Arg Glu Phe Val
885 890 895

Ser Ile Ser Ser Pro Ala His Val Ala Thr
900 905

<210> 259

<211> 1443

<212> DNA

<213> c-Cbl480

<220>

<221> CDS

<222> (1) .. (1440)

<223>

<400> 259

atg gcc ggc aac gtg aag aag agc tct ggg gcc ggg ggc ggc acg ggc 48
Met Ala Gly Asn Val Lys Lys Ser Ser Gly Ala Gly Gly Gly Thr Gly
1 5 10 15

tcc ggg ggc tcg ggt tcg ggt ggc ctg att ggg ctc atg aag gac gcc 96
Ser Gly Gly Ser Gly Ser Gly Gly Leu Ile Gly Leu Met Lys Asp Ala
20 25 30

ttc cag ccg cac cac cac cac cac cac ctc agc ccc cac ccg ccg 144
Phe Gln Pro His His His His His His His Leu Ser Pro His Pro Pro

35	40	45	
ggg acg gtg gac aag aag atg gtg gag aag tgc tgg aag ctc atg gac Gly Thr Val Asp Lys Lys Met Val Glu Lys Cys Trp Lys Leu Met Asp 50 55 60			192
aag gtg gtg cgg ttg tgt cag aac cca aag ctg gcg cta aag aat agc Lys Val Val Arg Leu Cys Gln Asn Pro Lys Leu Ala Leu Lys Asn Ser 65 70 75 80			240
cca cct tat atc tta gac ctg cta cca gat acc tac cag cat ctc cgt Pro Pro Tyr Ile Leu Asp Leu Leu Pro Asp Thr Tyr Gln His Leu Arg 85 90 95			288
act atc ttg tca aga tat gag ggg aag atg gag aca ctt gga gaa aat Thr Ile Leu Ser Arg Tyr Glu Gly Lys Met Glu Thr Leu Gly Glu Asn 100 105 110			336
gag tat ttt agg gtg ttt atg gag aat ttg atg aag aaa act aag caa Glu Tyr Phe Arg Val Phe Met Glu Asn Leu Met Lys Lys Thr Lys Gln 115 120 125			384
acc ata agc ctc ttc aag gag gga aaa gaa aga atg tat gag gag aat Thr Ile Ser Leu Phe Lys Glu Gly Lys Glu Arg Met Tyr Glu Glu Asn 130 135 140			432
tct cag cct agg cga aac cta acc aaa ctg tcc ctc atc ttc agc cac Ser Gln Pro Arg Arg Asn Leu Thr Lys Leu Ser Leu Ile Phe Ser His 145 150 155 160			480
atg ctg gca gaa cta aaa gga atc ttt cca agt gga ctc ttt cag gga Met Leu Ala Glu Leu Lys Gly Ile Phe Pro Ser Gly Leu Phe Gln Gly 165 170 175			528
gac aca ttt cgg att act aaa gca gat gct gcg gaa ttt tgg aga aaa Asp Thr Phe Arg Ile Thr Lys Ala Asp Ala Ala Glu Phe Trp Arg Lys 180 185 190			576
gct ttt ggg gaa aag aca ata gtc cct tgg aag agc ttt cga cag gct Ala Phe Gly Glu Lys Thr Ile Val Pro Trp Lys Ser Phe Arg Gln Ala 195 200 205			624
cta cat gaa gtg cat ccc atc agt tct ggg ctg gag gcc atg gct ctg Leu His Glu Val His Pro Ile Ser Ser Gly Leu Glu Ala Met Ala Leu 210 215 220			672
aaa tcc act att gat ctg acc tgc aat gat tat att tcg gtt ttt gaa Lys Ser Thr Ile Asp Leu Thr Cys Asn Asp Tyr Ile Ser Val Phe Glu 225 230 235 240			720
ttt gac atc ttt acc cga ctc ttt cag ccc tgg tcc tct ttg ctc agg Phe Asp Ile Phe Thr Arg Leu Phe Gln Pro Trp Ser Ser Leu Leu Arg 245 250 255			768
aat tgg aac agc ctt gct gta act cat cct ggc tac atg gct ttt ttg Asn Trp Asn Ser Leu Ala Val Thr His Pro Gly Tyr Met Ala Phe Leu 260 265 270			816
acg tat gac gaa gtg aaa gct cgg ctc cag aaa ttc att cac aaa cct Thr Tyr Asp Glu Val Lys Ala Arg Leu Gln Lys Phe Ile His Lys Pro 275 280 285			864

ggc agt tat atc ttc cgg ctg agc tgt act cgt ctg ggt cag tgg gct 912
 Gly Ser Tyr Ile Phe Arg Leu Ser Cys Thr Arg Leu Gly Gln Trp Ala
 290 295 300

att ggg tat gtt act gct gat ggg aac att ctc cag aca atc cct cac 960
 Ile Gly Tyr Val Thr Ala Asp Gly Asn Ile Leu Gln Thr Ile Pro His
 305 310 315 320

aat aaa cct ctc ttc caa gca ctg att gat ggc ttc agg gaa ggc ttc 1008
 Asn Lys Pro Leu Phe Gln Ala Leu Ile Asp Gly Phe Arg Glu Gly Phe
 325 330 335

tat ttg ttt cct gat gga cga aat cag aat cct gat ctg act ggc tta 1056
 Tyr Leu Phe Pro Asp Gly Arg Asn Gln Asn Pro Asp Leu Thr Gly Leu
 340 345 350

tgt gaa cca act ccc caa gac cat atc aaa gtg acc cag gaa caa tat 1104
 Cys Glu Pro Thr Pro Gln Asp His Ile Lys Val Thr Gln Glu Gln Tyr
 355 360 365

gaa tta tac tgt gag atg ggc tcc aca ttc caa cta tgt aaa ata tgt 1152
 Glu Leu Tyr Cys Glu Met Gly Ser Thr Phe Gln Leu Cys Lys Ile Cys
 370 375 380

gct gaa aat gat aag gat gta aag att gag ccc tgt gga cac ctc atg 1200
 Ala Glu Asn Asp Lys Asp Val Lys Ile Glu Pro Cys Gly His Leu Met
 385 390 395 400

tgc aca tcc tgt ctt aca tcc tgg cag gaa tca gaa ggt cag ggc tgt 1248
 Cys Thr Ser Cys Leu Thr Ser Trp Gln Glu Ser Glu Gly Gln Gly Cys
 405 410 415

cct ttc tgc cga tgt gaa att aaa ggt act gaa ccc atc gtg gta gat 1296
 Pro Phe Cys Arg Cys Glu Ile Lys Gly Thr Glu Pro Ile Val Val Asp
 420 425 430

ccg ttt gat cct aga ggg agt ggc agc ctg ttg agg caa gga gca gag 1344
 Pro Phe Asp Pro Arg Gly Ser Gly Ser Leu Leu Arg Gln Gly Ala Glu
 435 440 445

gga gct ccc tcc cca aat tat gat gat gat gat gat gaa cga gct gat 1392
 Gly Ala Pro Ser Pro Asn Tyr Asp Asp Asp Asp Asp Glu Arg Ala Asp
 450 455 460

gat act ctc ttc atg atg aag gaa ttg gct ggt gcc aag gtg gaa cgg 1440
 Asp Thr Leu Phe Met Met Lys Glu Leu Ala Gly Ala Lys Val Glu Arg
 465 470 475 480

tag 1443

<210> 260

<211> 480

<212> PRT

<213> c-Cbl480

<400> 260

Met Ala Gly Asn Val Lys Lys Ser Ser Gly Ala Gly Gly Gly Thr Gly
 1 5 10 15
 Ser Gly Gly Ser Gly Ser Gly Gly Leu Ile Gly Leu Met Lys Asp Ala
 20 25 30
 Phe Gln Pro His His His His His His His Leu Ser Pro His Pro Pro
 35 40 45
 Gly Thr Val Asp Lys Lys Met Val Glu Lys Cys Trp Lys Leu Met Asp
 50 55 60
 Lys Val Val Arg Leu Cys Gln Asn Pro Lys Leu Ala Leu Lys Asn Ser
 65 70 75 80
 Pro Pro Tyr Ile Leu Asp Leu Leu Pro Asp Thr Tyr Gln His Leu Arg
 85 90 95
 Thr Ile Leu Ser Arg Tyr Glu Gly Lys Met Glu Thr Leu Gly Glu Asn
 100 105 110
 Glu Tyr Phe Arg Val Phe Met Glu Asn Leu Met Lys Lys Thr Lys Gln
 115 120 125
 Thr Ile Ser Leu Phe Lys Glu Gly Lys Glu Arg Met Tyr Glu Glu Asn
 130 135 140
 Ser Gln Pro Arg Arg Asn Leu Thr Lys Leu Ser Leu Ile Phe Ser His
 145 150 155 160
 Met Leu Ala Glu Leu Lys Gly Ile Phe Pro Ser Gly Leu Phe Gln Gly
 165 170 175
 Asp Thr Phe Arg Ile Thr Lys Ala Asp Ala Ala Glu Phe Trp Arg Lys
 180 185 190
 Ala Phe Gly Glu Lys Thr Ile Val Pro Trp Lys Ser Phe Arg Gln Ala
 195 200 205
 Leu His Glu Val His Pro Ile Ser Ser Gly Leu Glu Ala Met Ala Leu
 210 215 220
 Lys Ser Thr Ile Asp Leu Thr Cys Asn Asp Tyr Ile Ser Val Phe Glu
 225 230 235 240
 Phe Asp Ile Phe Thr Arg Leu Phe Gln Pro Trp Ser Ser Leu Leu Arg
 245 250 255
 Asn Trp Asn Ser Leu Ala Val Thr His Pro Gly Tyr Met Ala Phe Leu
 260 265 270
 Thr Tyr Asp Glu Val Lys Ala Arg Leu Gln Lys Phe Ile His Lys Pro
 275 280 285
 Gly Ser Tyr Ile Phe Arg Leu Ser Cys Thr Arg Leu Gly Gln Trp Ala
 290 295 300
 Ile Gly Tyr Val Thr Ala Asp Gly Asn Ile Leu Gln Thr Ile Pro His
 305 310 315 320

Asn Lys Pro Leu Phe Gln Ala Leu Ile Asp Gly Phe Arg Glu Gly Phe
325 330 335

Tyr Leu Phe Pro Asp Gly Arg Asn Gln Asn Pro Asp Leu Thr Gly Leu
340 345 350

Cys Glu Pro Thr Pro Gln Asp His Ile Lys Val Thr Gln Glu Gln Tyr
355 360 365

Glu Leu Tyr Cys Glu Met Gly Ser Thr Phe Gln Leu Cys Lys Ile Cys
370 375 380

Ala Glu Asn Asp Lys Asp Val Lys Ile Glu Pro Cys Gly His Leu Met
385 390 395 400

Cys Thr Ser Cys Leu Thr Ser Trp Gln Glu Ser Glu Gly Gln Gly Cys
405 410 415

Pro Phe Cys Arg Cys Glu Ile Lys Gly Thr Glu Pro Ile Val Val Asp
420 425 430

Pro Phe Asp Pro Arg Gly Ser Gly Ser Leu Leu Arg Gln Gly Ala Glu
435 440 445

Gly Ala Pro Ser Pro Asn Tyr Asp Asp Asp Asp Asp Glu Arg Ala Asp
450 455 460

Asp Thr Leu Phe Met Met Lys Glu Leu Ala Gly Ala Lys Val Glu Arg
465 470 475 480

<210> 261

<211> 2721

<212> DNA

<213> human c-Cbl wild type ORF

<400> 261

```

atggccggca acgtgaagaa gagctctggg gccggggggcg gcacgggctc cgggggctcg      60
ggttcgggtg gcctgattgg gctcatgaag gacgccttcc agccgcacca ccaccaccac      120
caccacctca gccccaccc gccgggggacg gtggacaaga agatggtgga gaagtgtctg      180
aagctcatgg acaaggtggt gcggttgtgt cagaacccaa agctggcgct aaagaatagc      240
ccaccttata tcttagacct gctaccagat acctaccagc atctccgtac tatcttgtca      300
agatatgagg ggaagatgga gacacttgga gaaaatgagt attttagggt gtttatggag      360
aatttgatga agaaaactaa gcaaacata agcctcttca aggagggaaa agaaagaatg      420
tatgaggaga attctcagcc taggcgaaac ctaaccaaac tgtccctcat cttcagccac      480
atgctggcag aactaaaagg aatctttcca agtggactct ttcagggaga cacatttcgg      540
attactaaag cagatgctgc ggaattttgg agaaaagctt ttggggaaaa gacaatagtc      600

```

ccttggaaga gctttcgaca ggctctacat gaagtgcac ccacagttc tgggctggag 660
gccatggctc tgaaatccac tattgatctg acctgcaatg attatatattc ggtttttgaa 720
tttgacatct ttacccgact ctttcagccc tggctcctctt tgctcaggaa ttggaacagc 780
cttgctgtaa ctcatcctgg ctacatggct tttttgacgt atgacgaagt gaaagctcgg 840
ctccagaaat tcattcacia acctggcagt tatatcttcc ggctgagctg tactcgtctg 900
ggtcagtggg ctattgggta tgttactgct gatgggaaca ttctccagac aatccctcac 960
aataaacctc tcttccaagc actgattgat ggcttcaggg aaggcttcta tttgtttcct 1020
gatggacgaa atcagaatcc tgatctgact ggcttatgtg aaccaactcc ccaagaccat 1080
atcaaagtga cccaggaaca atatgaatta tactgtgaga tgggctccac attccaacta 1140
tgtaaaatat gtgctgaaaa tgataaggat gtaaagattg agccctgtgg acacctcatg 1200
tgcacatcct gtcttacatc ctggcaggaa tcagaaggctc agggctgtcc tttctgccga 1260
tgtgaaatta aaggctactga acccatcgtg gtagatccgt ttgatcctag agggagtggc 1320
agcctgttga ggcaaggagc agaggagct cctccccc aaattatgatga tgatgatgat 1380
gaacgagctg atgatactct cttcatgatg aaggaattgg ctggtgccaa ggtggaacgg 1440
ccgccttctc cattctccat ggccccacaa gcttcccttc ccccggtgcc accacgactt 1500
gaccttctgc cgcagcaggt atgtgttccc tcaagtgctt ctgctcttgg aactgcttct 1560
aaggctgctt ctggctccct tcataaagac aaaccattgc cagtacctcc cacacttcga 1620
gatcttcac caccacgcc tccagaccgg ccatattctg ttggagcaga atcccgacct 1680
caaagacgcc ccttgccctg tacaccaggc gactgtccct ccagagacaa actgccccct 1740
gtccccctca gccgccttgg agactcatgg ctgccccggc caatccccaa agtaccagta 1800
tctgccccaa gttccagtga tccctggaca ggaagagaat taaccaaccg gcactcactt 1860
ccattttcat tgccctcaca aatggagccc agaccagatg tgcttaggct cggaagcacg 1920
ttcagtctgg atacctccat gagtatgaat agcagcccat tagtaggtcc agagtgtgac 1980
caccclaaaa tcaaaccttc ctcatctgcc aatgccattt attctctggc tgccagacct 2040
cttctgtgc caaaactgcc acctggggag caatgtgagg gtgaagagga cacagagtac 2100
atgactccct cttccaggcc tctacggcct ttggatacat ccagagttc acgagcatgt 2160
gattgcgacc agcagattga tagctgtacg tatgaagcaa tgtataatat tcagtccag 2220
gcgccatcta tcaccgagag cagcaccttt ggtgaaggga atttggccgc agcccatgcc 2280
aacactggtc ccgaggagtc agaaaatgag gatgatgggt atgatgtccc aaagccacct 2340
gtgccggccg tgctggcccg ccgaactctc tcagatatct ctaatgccag ctctctcttt 2400

ggctggttgt ctctggatgg tgatcctaca acaaagtca ctgaaggttc ccaagttccc	2460
gagaggcctc caaaaccatt cccgcggaga atcaactctg aacggaaagc tggcagctgt	2520
cagcaaggta gtggtcctgc cgcctctgct gccaccgct cacctcagct ctccagtga	2580
atcgagaacc tcatgagtca ggggtactcc taccaggaca tccagaaagc tttggtcatt	2640
gccagaaca acatcgagat ggccaaaaac atcctcggg aatttgtttc cattttcttct	2700
cctgcccattg tagctaccta g	2721

INTERNATIONAL SEARCH REPORT

International application No.
PCT/AU2003/001676

A. CLASSIFICATION OF SUBJECT MATTER					
Int. Cl. ⁷ : C12N 15/00, C12Q 1/25, A01K 67/00					
According to International Patent Classification (IPC) or to both national classification and IPC					
B. FIELDS SEARCHED					
Minimum documentation searched (classification system followed by classification symbols) See electronic databases					
Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched See electronic databases					
Electronic data base consulted during the international search (name of data base and, where practicable, search terms used) WPDS MedLine CA: cbl gene/protein/oncogene, insulin/diabetes/glucose, metabolism/adiposity obesity/ fat deposition/appetite/food/feeding.					
C. DOCUMENTS CONSIDERED TO BE RELEVANT					
Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.			
X	Khan AH, Pessin JE. Insulin regulation of glucose uptake: a complex interplay of intracellular signalling pathways. Diabetologia. 2002 Nov. 45(11): 1475-83. 2002 Oct 18. Review.	All			
X	Liu Jun; Kimura Akiko; Baumann Christian A; Saltiel Alan R. APS facilitates c-Cbl tyrosine phosphorylation and GLUT4 translocation in response to insulin in 3T3-L1 adipocytes. Molecular and Cellular Biology, (2002 Jun). 22 (11) 3599-609.	All			
X	Yokoi Norihide; Komeda Kajuro; Wang He-Yao; Yano Hideki; Kitada Kazuhiro; Saitoh Yuka; Seino Yutaka; Yasuda Kazuki; Serikawa Tadao; Seino Susumu. Cblb is a major susceptibility gene for rat type 1 diabetes mellitus. Nature Genetics, (2002 Aug) 31 (4) 391-4.	All			
<input checked="" type="checkbox"/> Further documents are listed in the continuation of Box C <input type="checkbox"/> See patent family annex					
<table style="width: 100%; border: none;"> <tr> <td style="width: 33%; vertical-align: top;"> <p>* Special categories of cited documents:</p> <p>"A" document defining the general state of the art which is not considered to be of particular relevance</p> <p>"E" earlier application or patent but published on or after the international filing date</p> <p>"L" document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)</p> <p>"O" document referring to an oral disclosure, use, exhibition or other means</p> <p>"P" document published prior to the international filing date but later than the priority date claimed</p> </td> <td style="width: 33%; vertical-align: top;"> <p>"T" later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention</p> <p>"X" document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone</p> <p>"Y" document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art</p> <p>"&" document member of the same patent family</p> </td> <td style="width: 33%;"></td> </tr> </table>			<p>* Special categories of cited documents:</p> <p>"A" document defining the general state of the art which is not considered to be of particular relevance</p> <p>"E" earlier application or patent but published on or after the international filing date</p> <p>"L" document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)</p> <p>"O" document referring to an oral disclosure, use, exhibition or other means</p> <p>"P" document published prior to the international filing date but later than the priority date claimed</p>	<p>"T" later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention</p> <p>"X" document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone</p> <p>"Y" document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art</p> <p>"&" document member of the same patent family</p>	
<p>* Special categories of cited documents:</p> <p>"A" document defining the general state of the art which is not considered to be of particular relevance</p> <p>"E" earlier application or patent but published on or after the international filing date</p> <p>"L" document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)</p> <p>"O" document referring to an oral disclosure, use, exhibition or other means</p> <p>"P" document published prior to the international filing date but later than the priority date claimed</p>	<p>"T" later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention</p> <p>"X" document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone</p> <p>"Y" document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art</p> <p>"&" document member of the same patent family</p>				
Date of the actual completion of the international search 23 January 2004		Date of mailing of the international search report 30 JAN 2004			
Name and mailing address of the ISA/AU AUSTRALIAN PATENT OFFICE PO BOX 200, WODEN ACT 2606, AUSTRALIA E-mail address: pct@ipaustalia.gov.au Facsimile No. (02) 6285 3929		Authorized officer Gillian Allen Telephone No : (02) 6283 2266			

INTERNATIONAL SEARCH REPORT

International application No.

PCT/AU2003/001676

C (Continuation). DOCUMENTS CONSIDERED TO BE RELEVANT		
Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	Chiang SH, Baumann CA, Kanzaki M, Thurmond DC, Watson RT, Neudauer CL, Macara IG, Pessin JE, Saltiel AR. Insulin-stimulated GLUT4 translocation requires the CAP-dependent activation of TC10. Nature, 2001 Apr 19; 410(6831): 944-8.	All
X	Ahmed Z, Smith BJ, Pillay TS. The APS adapter protein couples the insulin receptor to the phosphorylation of c-Cbl and facilitates ligand-stimulated ubiquitination of the insulin receptor. FEBS Lett. 2000 Jun 9; 475(1): 31-4.	All
X	Baumann CA, Ribon V, Kanzaki M, Thurmond DC, Mora S, Shigematsu S, Bickel PE, Pessin JE, Saltiel AR. CAP defines a second signalling pathway required for insulin-stimulated glucose transport. Nature. 2000 Sep 14; 407(6801): 202-7.	All